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ALIGNMENTS

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1 HSM802204 LOCUS SOURCE ORGANISM COMMENT DEFINITION JOURNAL TITLE Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S. Direct Submission
Submitted (15-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium of the German Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 4695 bp mrNA linear PRI 18-FEB-200 HOMO sapiens mrNA; cDNA DKFZp434M0223 (from clone DKFZp434M0223); AL137479 Genome Project AL137479.1 GI:6808092 This clone (DKFZp434M0223) is available at the RZPD in Berlin. human. (bases 1 to 4695) PRI 18-FEB-2000

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                                                      CGTTGTCCTGCTGGTTTTGGAGATCTCAACTCTGGCTGTGTACCGATTGCCACACCCCAGG 445
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please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/.
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/db_xref="taxon:9606"
/clone="DKPTp434M0223"
/tissue_type="testis"
/clone_lib="434 (synonym: htes3). Vector pSport1; host
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gfleghyyfdylgnlialanilysicytflyllalbutlpaerddfilgilwcyfivytlle

MLTKVFALGLRGYLSYPSNVFDGLLTVVLLVLEISTLAVYRLPHPGWRPEMVGLLSLW

DMTRKLNMLTYFRFELRITESNKFMAVVASTVLGLVQNNRAFGGILVVVYYVFAIIGIN

LFRGVTVALFCNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLMNLMVVNNWQV

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JOURNAL Unpublished (2000) REFERENCE 2 (bases 1 to 2200) RIFERENCE Isogai, T. and Otsuki, T. TITLE Direct Submission Submitted (23-AUG-2000) Kisarazu, Chiba 29-081 Tel:81-438-52-3951, Fax NEDO human CDNA sequency International Trade and sequencing: Research As construction, 5'- & 3'- Helix Research Institut	RESULT 2 AK023366 AK023366 AK023366 DEFINITION ACCESSION ACCESSION AK023366.1 GI:10435270 VERSION AK023366.1 GI:10435270 VERSION AK023366.1 GI:10435270 VERSION AK023366.1 GI:10435270 VERSION AK023366.1 GI:10435270 CORGANISM Homo sapiens cution sapiens EUKaryota; Metazoa; Chord Mammalia; Eutheria; Prima REFERENCE 1 (sites) AUTHORS Isogai, T., Ota, T., Hayash Nishikawa, T., Nagai, K., Sugawara, M., Takahashi, M. Sugawara, M., Takahashi, M. Cono, Y., Takiguchi, S., Wat Ishii, S., Kawai, Y., Saito, Nakamura, Y., Nagahari, K.,	Db 986 CCTTGCTGGAGCCCCAGAGGC Qy 1386 TCTGGAGGAGCCCGGGGAGGA Qy 1486 TCTGGAGGAGCCCGAGGAGGA Db 1046 TCTGGAGGAGCCCGAGGAGAGA Qy 1446 GCTGTGCAGGTGA 1458	1266 926 1326	Qy 1146 GATGGTGGTGAACAACTGGCA	1086 746	Qy 1026 TGGAAACAGCAGCCTGGCCCC	Db 626 CTACTACGTATTTGCCATCAT
to human cDNA sequencing project by histshed (2000) (bases 1 to 2200) (gai,T. and Otsuki,T. gai,T. and Otsuki,T. mitted (23-AuG-2000) to the DDBJ/EMBL/GenBank databases. Takamitted (23-AuG-2001) to the DDBJ/EMBL/GenB	AKO23366 AKO23366 AKO23366.1 GI:10435270 AKO23366.1 GI:10435270 Oligo capping; fis (full insert sequence). Homo sapiens ovary, tumor tissue cDNA to mRNA, clone_lib:OVARCl Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (sites) Nishikawa, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Joho, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yanamamoto, J., Wakamatsu, A., Ishii, S., Kawai, Y., Saito, K., Yanamamoto, J., Wakamatsu, A., Ishii, S., Kawai, Y., Saito, K., Yanamamoto, J., Wakamatsu, A., Ishii, S., Kawai, Y., Saito, K., Masuho, Y., Ninomiya, K. and Iwayanagi,	CCTTGCTGGGACCCAGAGGCCACCTACCAGATGACTGTGAGCTCCTCTCAGGGACCCCAGAGGCCACCACCAGATGACTGTGAGCTCCAGCAGCACCAGGGATAT TCTGGAGGAGCCCGGGGAGGATGAGCTCACCAGAGAGGCTGAGCCAGCACCCGCACCTGTG	TOTAL TO THE PROOF OF THE PROOF	GATGGTGGTGAACAACTGGCAGGTGTTTCTGGATGCATATCGGCGCTACTCAGGCCCGTG [GGAGTACTGGGCCAACAACTTCGATGACTTTGCGGCTGCCCTGGTCACTCTGTGGAACTT 	TGGAAACAGCAGCCTGGCCCTGCCAATGGCTCGGCGCCCTGTGGGAGCTTCGAGCAGCT 	TACTACGTATTTGCCATCGTTGGGATCAACTTGTTTAGAGGCGTCATTGTGGCTCTTCC

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                                                                                                                                                                                                                                                                                Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 147224)
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HOMO Sapiens DNA, clone:RP11-40B5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 etc.) and Department of Virology, Institute of Medical Science,
                                                                                            Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                             Center clone name: RP11-40B5
                                                             Center project name: HumDraftll
         Sequencing vector:
                                                                                                                                          Center code: RIKEN
                                                                                                                                                      Center: RIKEN Genomic Sciences Center(GSC)
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/note="cloning vector: pME18SFL3"
635 c 671 g 511 t
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/clone_lib="OVARC1"
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/db_xref="taxon:9606"
                                                                                 --- Project Information
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--- Summary Statistics
ing vector: PCR products; 100% of reads
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99.1%;
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                                                                                                                                                                              Genome Center
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Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 141612 bases at least Q40
Consensus quality: 144511 bases at least Q30
Consensus quality: 145118 bases at least Q20
Insert size: 145424; sum-of-contigs
Quality coverage: 6.27x in Q20 bases; sum-of-contigs
Quality coverage: 6.27x in Q20 bases; sum-of-contigs
NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved
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16213 contig of 16213 bp in length
36641 36540 contig of 20227 bp in length
36641 36540 contig of 12797 bp in length
53479 66275 contig of 12797 bp in length
66376 80746 contig of 12797 bp in length
80847 91853 contig of 11007 bp in length
100860 107681 contig of 6822 bp in length
110782 114540 contig of 6759 bp in length
114641 120591 contig of 5055 bp in length
1120692 126296 contig of 5605 bp in length
1132087 130100 contig of 2684 bp in length
1132287 13718 contig of 2734 bp in length
1132285 135718 contig of 2734 bp in length
113285 135718 contig of 2734 bp in length
1135819 138905 contig of 3087 bp in length
1145037 147244 contig of 3087 bp in length
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16214 16313: gap of 100 bp
16314 36540: contig of 20227 bp in length
36541 36640: gap of 100 bp
36641 5378: contig of 16738 bp in length
53479 53478: gap of 100 bp
66276 66275: contig of 12797 bp in length
66276 66375: gap of 100 bp
66376 80746: contig of 14371 bp in length
80747 80846: gap of 100 bp
80847 91853: contig of 1100 bp
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114641 120591
114641 120591
120592 120691:
120692 126296:
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107782 11454
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100860 10768;
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100759; contig of 8806 bp
100859; gap of 100 bp
107681; contig of 6822 bp
107781; gap of 100 bp
114540; contig of 6759 bp
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140559: contig of 1554 bp in length
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contig of 6759 br
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FEATURES
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                                                                                                      Db 117656 TGGAGCTGCCGCTTCTGCTCTTAGCAGGATGATGGGCCAGGACAGGGAGGAGGCTGACCTAC
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                                                   181 TTCCAGAACCTGCCTGAGTCTCTGACTTCCCTCCTGGTGCTGACCACCGGCCAACAAC 240
                                                                                                                                     121 TGGAGCTGCCGCTTCTGCTCTCAGCAGGATGATGGGCAGGACAGGGGAGAGGGCTGACCTAC 180
                                                                                                                                                                                                                                                                       61 CCAACCGGTTGGGTCCGGGGCCTGGAGCTCAGCCTGTGGGGTGGGGACCCAGTGGTGCCC 120
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100860. .107681
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/chromosome="11"
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145037. .147224
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114641. .120591
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139006. .140559
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132985. .135718
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99.2%;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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186974 bp DNA linear H1 H0MO sapiens chromosome 11 clone RP11-554A11 map 11q, SEQUENCE, 31 unordered pieces.
AP003071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-DEC-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AP003071.1 GI:12248744
Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 179023 bases at least 040 consensus quality: 182104 bases at least 030 consensus quality: 183462 bases at least 020 Insert size: 183974; sum-of-contigs quality coverage: 9.07x in 020 bases; sum-of-contigs quality coverage: 9.07x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                    Center project name: HumDraftll Center clone name: RP11-554A11
                                                                                                                                                                                                                                                                                                                                                                                                                                          web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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sapiens DNA, clone:RP11-554A11.
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                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
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182351 contig of 1962 bp in length
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138410 143433; contig of 5024 bp in.

144344 143533; gap of 100 bp
149592 149791; gap of 100 bp
153822 153921; gap of 100 bp
153922 159279; contig of 6158 bp in length
59280 159379; gap of 100 bp
162427; contig of 5358 bp in length
48 165257; gap of 100 bp
166045; gap of 100 bp
168880; gap of 100 bp
169400; gap of 100 bp
171169; contig of 7375 bp in length
169400; gap of 100 bp
172788; contig of 1769 bp in 1°
172788; contig of 100 bp
172788; contig of 1769 bp in 1°
188; gap of 100 bp
172788; contig of 1769 bp in 1°
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39912 40011: gap of 100 bp
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56822 56921: gap of 100 bp
56922 56921: gap of 100 bp
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3316: gap of 100 bp
106242: contig of 10926 bp in length
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115023 115122: gap of 100 bp 115123 120641: contig of 5519 bp

in

120642 120741: gap of 120742 127870: cont

120741: gap of 100 bp in 127870: conting of 7129 bp in 127970: gap of 100 bp in 133204: conting of 5234 bp in 133304: gap of 100 bp in 138309: conting of 5005 bp in 128309: conting of 50

106243 106342: gap of 106343 115022: cont

100 bp

169301 169400: gap of
169401 171169: contig of 1769 bp in
171170 171269: gap of 100 bp
171270 172788: contig of 1519 bp in
172789 172888: gap of 100 bp
172889 174327: contig of 1439 bp in
174328 174427: gap of 100 bp
174428 176380: contig of 1953 bp in

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176381 176480:

6480: gap of 178019: contig

of.

100 bp 1539 bp

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178119: gap

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                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-primer ET; 88% of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 174246 bases at least Q40
Consensus quality: 180170 bases at least Q30
Consensus quality: 180170 bases at least Q30
Consensus quality: 183510 bases at least Q20
Insert size: 197000; agarose-fp
Insert size: 197100; agarose-fp
Quality coverage: 3.73 in Q20 bases; agarose-fp
Quality coverage: 3.93 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGATG 141585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; 88%
Sequencing vector: plasmid; 12%
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Web site:http://genome.wustl.edu/gsc/index.shtml
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Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 194781)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 11 clone RP11-554A11, WORKING DRAFT SEQUENCE, 27 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH0554All
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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AC019124.4 GI:8568923
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                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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2472
4257
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, 2000 this sequence version replaced gi:7408149.
1121: contig of 1121 b.
1221: gap of unknown 1.
2371: contig of 1150 b.
2471: gap of unknown 1.
4256: contig of 1785 b.
4356: gap of unknown 1
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18929. .22949
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15417. .18828
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12343. .15316
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1222. .2371
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165048: contig of 13364 b
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178773: contig of 13625 b
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41346. .47770
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81173. .91442
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47871, .54230
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165149. .178773
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112934. .126132
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30558. .35980
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151685. .165048
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126233. .137943
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                                                                                                                                                                           three spined stickleback.

Gasterosteus aculeatus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Euteleostei; Neoteleostei; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                             G72237 520 bp r Stn17 Stickleback cDNA Gasterosteus 65-32/T3, sequence tagged site.
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Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B.
                                                                                                                                                                                                                                                                                                                                   G72237
G72237.1 GI:17977097
STS.
                      1 (bases 1 to 520)
Peichel,C.L., Nereng,K.S., Ohgi,K.A., Cole,B.L., Colosimo,P.F.,
Buerkle,C.A., Schluter,D. and Kingsley,D.M.
The genetic architecture of divergence between threespine
stickleback species
                                                                                                                                                    Gasterosteidae;
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Pred. No. 1.2e-40;
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                             AGCCGCCACACCACTGATTGGTCGAAGATCTACTTTGTGTTGGTGGCTCACCTCCTCG
                                                                                       ATCATGTTGCTGTACAACGTCATGGTGGTGTACAACTGGCAGGCCTTCCTGGAAGCATAC 139
                                                                                                                                                  TGTGGCACCTACGAGCAGCTGGAATACTGGCCAAACAACTTTGATGACTTTGCTGCCGCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: David M. Kingsley
Dept of Developmental Biology/ Howard Hughes Medical Institute
Stanford University School of Medicine
B300 Beckman Center, 279 Campus Drive, Stanford, CA 94305-5329,
Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buffer:
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PCR cycles:
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/lab.host="XII-Blue MRF/"
/note="Vector: ZAP Express; V-type: Phage; Oligo(dT)
primed cDNA unidirectionally cloned into the EcoRI/XhoI
sites of ZAP Express."
                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Head and internal organs"
/clone_lib="Stickleback cDNA"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Salinas River,
/db_xref="taxon:69293"
/clone="65-32/T3"
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                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; 88%
Sequencing vector: plasmid; 12%
Sequencing vector: plasmid; 12%
Chemistry: Dye-primer ET; 88% of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 174246 bases at least Q40
Consensus quality: 180170 bases at least Q30
Consensus quality: 180510 bases at least Q20
Insert size: 197000; agarose-fp
Ouality coverage: 3.73 in Q20 bases; sum-of-contigs
Quality coverage: 3.93 in Q20 bases; sum-of-contigs
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                                                                                                                                                      * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently 
* consists of 27 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7408149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0554A11
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
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be preserved.
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1121: contig of 1121 bp in length
1221: gap of unknown length
2371: contig of 1150 bp in length
2471: gap of unknown length
4256: contig of 1785 bp in length
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/db_xref="taxon:9606"
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4: contig of 1341 bp in
4: gap of unknown length
5: contig of 13364 bp in
6: contig of 13364 bp in
7: contig of 13625 bp in
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contig of 8100 bp in length
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of 2974
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Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                 AC098981
AC098981.3 GI:17975740
HTG; HTGS_PHASE1.
                                                                                                                  AC098981 162797 bp DNA Rattus norvegicus clone CH230-112J19, ***
***, 73 unordered pieces.
                                                                                                                                                                                                                             17266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45508
                                                                                                               73 unordered pieces.
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a 50858 c 51838 g
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178874. .194781
note="assembly_name:Contig32
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91543. .101161
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81173. .91442
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112934. .126132
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101262. .112833
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63906. .72872
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54331, .63805
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47871. .54230
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25949. .30457
/note="assembly_name:Contig16"
30558. .35980
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126233. .137943
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72973. .81072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig17"
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REFERENCE

AUTHORS

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Dugan, A.L., Dilly, H., Dull, H.R., Dull, Levis, J., Dugar, Accha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguro, D., Flagg, N., Ford, J., Foster, P., Garia, A., Gao, J., Garcia, A., Garner, T., Foster, P., Gall, R., Gaorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, C., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lux, L., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lux, L., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Martiney, E., McLeod, M. P., Meador, M., Morris, S., Moser, M., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Drimus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Suton, A., Svatek, A., Tabor, P., Tamerisa, K., Tang, H., Shooshtari, N., Walliams, S., Walliamson, A., Washington, C., Walliams, G., Walliamson, A., Washington, C., Walliams, G., Williamson, A., Washington, C., Walliams, G., Williamson, A., Washington, C., Walliams, G., Williamson, A., Washington, C., Walliamson, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny,D.M., Adams,C., Adio-oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,M.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,R.L., Ding,Y., Dinh,H.H., Douthwalte,K.J., Draper,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus.
1 (bases 1 to 162797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baylor Plaza, Houston, TX 77030, USA
On Dec 21, 2001 this sequence version replaced gi:17062421.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 73 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                                           Consensus quality: 121859 bases at least Q40 Consensus quality: 132629 bases at least Q30 Consensus quality: 141983 bases at least Q20 Consensus quality: 141983 bases at least Q20 Estimated insert size: 1310105; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: CH230-112J19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ Genome Center
Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329First call to
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65479 67636 67736

gap of contig

unknown of 1696 unknown of 2263

length

69999

70099

71895 74076

94342

gap of contig gap of contig

unknown of 2150 unknown of 1943 unknown of 1664

unknown

length

length

length

gap of contig gap of contig gap of contig gap of contig

of 1118 unknown

bp in l

length

of 2018 of 1909

bp in l bp in l

of

length

81658 81758 84092 84192 86276 86376

gap of contig

bp in length length bp in length length

8409

gap of contig gap c gap of contig

of

unknown

length

length length

of 2084

bp in l bp in l

in length

unknown of 2335

of 1796

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in length in length

length

unknown

length

76000 77327

74176 75900

75999

unknown of 1724

of 2181

unknown

ength

of 1327

bp in l bp in l

length length length 59837 62600 62700

65379

gap of contig gap of contig

of 2679 unknown of 2763 unknown

bp in length

in length in length

length length

of 2157

length

length

length

in length

56664 52661 56564

gap of contig contig gap of contig

unknown of 3073

of 3903 unknown of 3026

in length in length

bp in . length

Length Length

gap of contig

46878 46978 49435 49535 52561

gap of contig gap of contig

of 2457 of 2238 of 3238

44540 44640

35573 38724 38824 41202 41302

30886 26329 22043 22143

gap of

unknown of 3151

of 4487 of 4457 of 4186

unknown unknown unknown

gap of

unknown of 2378

ength _ength ength

gap of

unknown

length

conti

unknown

ength

length length length

bp in length

26429

contig

gap of contig

gap of unknown contig of 5064

length

length

length

length

length length

Length

length

gap of unknown contig of 4586

12193 12293 16879 16979

JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAL

COMMENT

5958 6058 contig of 6135 of 5957 bp in length length length

ranbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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RESULT 10
AC098981
             REFERENCE
                                                                                VERSION
                                                                      KEYWORDS
                                                                                           ACCESSION
                                                                                                               DEFINITION
     AUTHORS
                                                     ORGANISM
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                    62538 TCTACCACAGCAACGTGTTCGATGGCCTCCTGACCATCATCCTGCTGG 62491
                                                                                                                                                                                                          62598 TGTACTACCTGCTGGAGCTGCTGTTCAAGGTGTTCGCGCTGGGCCTACGGGGCTACCTGT 62539
                                                                                                                                                                              742 CCTACCCCAGCAACGTGTTTGACGGGCTCCTCACCGTTGTCCTGGTGG 789
                                                                                                                                                                                                                     682 TGTACTACCTGTTGGAGTTGCTGCTCAAGGTCTTTGCCCCTGGGCCTGCGAGGGTACCTGT 741
                                                                                                                                                                                                                                                              Local Similarity
  Muzny, D.M., Adams, C.,
                                                                                                                                                                                                                                                     90;
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                              AC098981.3 GI:17975740
                      Rattus.
                                                 Norway rat.
Rattus norvegicus
                                                                     HTG; HTGS_PHASE1.
                                                                                          AC098981
                                                                                                             Rattus
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Adio-Oduola, B., Ali-osman, F.R., Allen, C.
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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Bscotto, M., Falls, T., Ferraquto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garzia, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Harris, C., Harris, G., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homai, F., Howard, S., Huber, J., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., Michel, T., Meddor, M., Morgan, M., Morris, S., Moser, M., Nickerson, E., Neckens, R., Pathus, E., Pace, A., Paycon, B., Pecry, J., Peters, L., Peters, L., Pill, J., Li, Martin, R., Rojubokan, I., Rolfe, M., Nickens, R., Sodergren, E., Sonatke, T., Sparks, A., Stanley, H., Tansey, J., Taylor, C., Taylor, P., Tamerisa, K., Tang, H., Stanley, H., Tansey, J., Taylor, C., Taylor, P., Tamerisa, K., Tang, H., Stanley, H., Washen, R., Wangles, L., Veta, V., Villalon, D., Vinson, R., Morley, R., Wangles, L., Veta, V., Villalon, D., Vinson, R., Wallans, O., A., Walland, R., Washington, C., Walliams, G., Williams, G., Williamson, A., Waleczyk, R., Wooden, S., Walland, S., Walson, D., Walson, D., Walson, D., Walson
                                                                                                            Direct Submission
Submitted (08-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 21, 2001 this sequence version replaced gi:17062421.
                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Center: Baylor College of Medicine Center code: BCM
                                                                                   - Genome Center
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COMMENT

REFERENCE TITLE JOURNAL

TITLE AUTHORS JOURNAL

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Center clone name: CH230-112J19 Center project name: GGNZ Project Information

밁 Š 망 δõ

findPhrapList Assembly program: Phrap; version 0.990329First call to ---- Summary Statistics

Consensus quality: 121859 bases at least Q40 Consensus quality: 132629 bases at least Q30 Consensus quality: 141983 bases at least Q30 Estimated insert size: 130105; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 73 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence _data.html).

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COMMENT
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Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
MacLean,C., Maddonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., NayJor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson, Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Changarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Gindes,S., Goyette,M., Graham,L., Grand-Dierro N Hance D Hasford N Horton I Halme W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-APR-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the record is updated, the accession number will
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Center clone name: 160_D_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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3197: contig of 733
3297: gap of 100 bp
4018: contic - 7
                                                                                       8218:
                                                                                                                                                                                                                        5745:
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2464: gap of 10
3197: contig of
  9838:
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8958:
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8118:
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9: contig of 721
p of
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contig
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contig of 703 k
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15464 15563: gap of 100 bp 11564 16274: contig of 711 bp in length 16275 16374: gap of 100 bp 116375 17086: contig of 712 bp in length 17087 17186: gap of 100 bp 17927 18026: gap of 100 bp 18027 18026: gap of 100 bp 18027 18026: gap of 100 bp 18687: gap of 100 bp 18868 19588: contig of 741 bp in length 19589 19688: gap of 100 bp 19589 19688: gap of 100 bp 19689 20403: contig of 721 bp in length 20504 21214: contig of 715 bp in length 21315 21314: gap of 100 bp 22138 22137: gap of 100 bp 22138 22137: gap of 100 bp 22138 22137: gap of 100 bp 22138 22863: contig of 726 bp in length 22664 22963: gap of 100 bp 22964 2363: gap of 100 bp 22964 22963: gap of 100 bp 22964 22964 22963: gap of 100 bp 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 22964 229
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12258 12953: contig of 696 b
12954 13053: gap of 100 bp
13054 13787: contig of 734 b
13788 13887: gap of 100 bp
1388 14618: contig of 731 b
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37735 37834:
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33664 33763: gap of 1
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10606: gap of 100 bp
11347: contig of 741 bp in length
11447: gap of 100 bp
12157: contig of 710 bp in length
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24625: gap of 100 bp
25366: contig of 741 bp in length
25466: gap of 100 bp
26205: contig of 739 bp in length
26305: gap of 100 bp
27052: contig of 747 bp in length
27152: gap of 100 bp
27152: gap of 100 bp
27894: contig of 742 bp in length
27994: gap of 100 bp
27894: contig of 702 bp in length
27994: gap of 100 bp
27894: contig of 688 bp in length
28796: gap of 100 bp
                                                                                                                                                                        5393: gap of 100 bp
36114: contig of 721 bp
6214: gap of 100 bp
36950: contig of 736 bp
7050: gap of 100 bp
37734: contig of 684 bp
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30320: contig of 726 bp
0420: gap of 100 bp
31155: contig of 735 bp
1255: gap of 100 bp
31984: contig of 729 bp
                                                                                                                                                                                                                                                                                                             34400.
63: gap of 100 bp
35293: contig of 730 bp
44: gap of 100 bp
39357: contig of 713 bp
57: gap of 100 bp
40180: contig of 723 bp
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38544: contig of 710
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32814: contig of 730 bp
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99: gap of 100 hr
24575:
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GGCCAACAACTTCGATGACTTTGCGGCTGCCCTGGTCACTCTGTGGAACTTGATGGTGGT 1154
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                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2742)
Perelygin, A.A. and Brinton, M.A.
Touchtional cloning of the Flv gene
                                                                                                                                                                                                                                                                                            Mus musculus calcium channel mRNA, AF217002
                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                        AF217002.1
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Perelygin,A.A.
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                                                                                                                                                                                                                        house mouse
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  (bases 1 to 2742)
celygin, A.A. and B
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43488: cont
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41017: con
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57462:
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; gap of
42653;
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76.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45094; contig of 715 bp in 94; gap of 100 ho 45938; con+'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138: gap of 100 bp 56662: contig of 724 bp 62.
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54177: contig of 740 bp in length
77: gap of 100 bp
55026: contig of 749 bp in length
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14279: contig of 691 bp in length
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     Brinton, M.A.
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contig of 747 bp in
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contig of 726 bp in
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contig of 700 bp
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of 737 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153;
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Submitted (16-DEC-1999) Biology, Georgia State University, 24
Peachtree Center Ave, Atlanta, GA 30303, USA
Location/Qualifiers
                              AB018253.1 GI:4586962 voltage-gated ca channel.
                                                                              Rattus norvegicus mRNA for voltage-gated ca channel, \tt AB018253
       Rattus norvegicus kidney cDNA to mRNA
                                                                                                                                AB018253
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YYYLNNFDNILNSFVTLFELTVVNNWYIIMEGVTSQTSHWSRLYFMTFYIVTMVVMTI
IVAFILEAFVFRMNYSRKSQDSEVDSGIVIEKEMSKEELMAVLELYREERGTSSDVTR
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VVAVNGVWILVETFMLKGGNFTSKHVPWSYLVFLTIYGVELFMKVAGLGPVEYLSSGW
NLFDFSVTAFAFLGLLALTLNMEPFYFIVVLRPLQLLKLFKLKKRYRVVLDTMFELLP
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LLTTANFPDVMMPSYSRNPWSCVFFIVYLSIELYFIMNLLLAVVFDTFNDIEKHKFKS
LLLHKRTAIQHAYGLLASQRRPAGISYRQFEGLMRFYKPRMSARERFLTFKALNQSNT
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HNSQVPSLYSGADSPBSSPTGHNWEMNYGDAAYIL
FYHNHETYMBELTTALLLLLISLCSBPAVPULKLHTYVHATLELFALMYVVFELCMKL
RWLGFHTFVRHKRTMVKTSVLVVQFIBAIVVLVRQTSHVRVTRALRCIFLVDCRXCGG
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819 c 727 g
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/note="similar to Rattus norvegicus voltage-gated calcium
channel mRNA deposited in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAG44100.
/db_xref="GI:12004581"
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L. .2742
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Pred. No. 0.0006
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RESULT 12 AF217002 LOCUS

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REFERENCE

AUTHORS JOURNAL REFERENCE

ROD 09-MAY-2000

complete cds.

AUTHORS TITLE

SOURCE VERSION ACCESSION DEFINITION

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Query Match Best Local S Matches 84

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                                               1101 ACTTTCCAGACGTCATGATGCCCTCCTACTCCCGGAACCCCTGGTCCTGTGTCTTTTA
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                                                                                                                                 ACACCTTCAACGACATCGAAAAGCACAAGTTCAAGTCCTTGCTGCATCAAGCGAACAG
                                                                                                                                                                            GTCAGTTCCGGGGCTACCTGATGAAATCTCTCCAGACCTCGCTGTTTCGGAGGCGGCTGG
                                                                                          GAACCCGGGCTGCCTTTGAAGTCCTATCCTCCATGGTGGGGGAGGAGGAGCCCTTC 471
                                                                                                                                                                                                                     TCGTGTACCTCTCCATTGAGCTGTACTTCATCATGAACCTGCTCCTAGCCGTGGTGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150;
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Submitted (02-OCT-1998) Kenichi Ishibashi, Jichi Medical School, Pharmacology; Minami-Kawachi, Kawachi, Tochigi 329-0498, Japan (E-mail:kishibasjichi.ac.jp, Tel:81-285-58-7326,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishibashi,K., Suzuki,M. and Imai,M. Molecular cloning of a novel form (Two-repeat) protein related voltage-gated sodium and calcium channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRLLDTLSQMEKYQQNSMVFLGRQSRTKSDLSLKMYQEEIQEWYEEHAREQEQQQLRGSAPSFAAQQTPGSRQRSQTYT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLEDFSLTAFAFLGLLALTLINMEPFYFTVVLRPLQLLRLFKLKKRYRNVLDTMFELLP
RMASLGLTLLTFYYSFAIVGMEFFSGRLSPNCSTPARWGLTPIDSSITRLGNKTKFGR
KGYYYLNNFDNILNSFYTLFELTVVNNWYIIMEGVTSQTSHWSRLYFMTFYIVTMVVM
TIIVAFILEAFVFRMNYSRKSQESEVDSGIVIEKEMSKEELLAILELHREARGTSSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLLSLKDFYDIYEVAALQWKAKKNRQHWEDELPRTAFLIFKGINILVNSKAFQYFMYL
VVAVNGVWILVETFMLKGGNFISKHVPWSYLVFLTIYGVELFMKVAGLGPVEYLSSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RWLGFHTFVRHKRTMVKTSVLVVQFIEAIVVLVRQTSHVRVTRALRCIFLVDCRYCGG
VRRNLRQIFQSLPPFMDILLLLLFFMIIFAILGFYLFSTNPSDPYFNTLENSIVNLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSVILDDDVLLILTLDEELSAPLTDSNGLGQEDLPSKNGGGQSG
PNSQVPSLVSGADSPPSSPPGHNWEMNYQEAAIYLQEGQNNDKFFTHPKDARALAAYL
FVHNHFFYMMELLTALLLLLLSICESPAVPALKLRTYVHATLELFALMYVVFELCMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  updated (27-Nov-1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLTTANEPDVMMPSYSRNPWSCVFFTVYLSIELYFIMNLLLAVVFDTFNDIEKHKFKS
LLLHKRTATOHAYHLLVSORRPAGISYROFEGLMRFYKPRMSARERFLTFKALNOSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="voltage-gated ca channel"
/protein_id="BAA76556.1"
/db_xref="GI:4586963"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
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ACCESSION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                 1071 GAGCTTCGAGCAGCTGGAGTACTGGGCCAACAACTTCGATGA 1112
                                                                                                 1011 CATTGTGGCTCTTCCTGGAAACAGCAGCCTGGCCCTGCCCAATGGCTCGGCGCCCTGTGG 1070
     869
                                                                                                                                                                   951 GATCCTGGTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGCGT 1010
                                                                                                                                                                                                           689 CGTGCCTAGCATGCGGATCCTGGTCACTCTGCTGCTGGATACGCTGCCCATGCTCGGGAA 748
                                                                                                                                                                                                                                            831 CCGCATGCTGAACATGCTCATCGTGTTCCGCCTTCCTGCGTATCATCCCCAGCATGAAGCC 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 ATCCTGGAGGCCTTTGACGCCTTCATTTTCGCCTTTTTTTGCGGTGGAGATGGTCATCAAG
                                                                                                                                                                                                                                                                                                                                                                                      771 CTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGAC 830
                                                                                                                                                                                                                                                                                                                                                                                                                           516 ATGGTGGCCTTGGGGCTGTTCGGGCAGAAGTGTTACCTGGGTGACACGTGGAACAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         711 GTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGACGGGCTC 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 651 ATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 CTCTTCGGCCACTACTACTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTG 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCTCGGCTATCAGGACCG-----TGCGGGTGCTGCGGCCCCTCCGCGCCATCAACCG 688
                                                                                                                                                                                                                                                                                                                                                    GATTTCTTCATCGTCGTGGCGGGC-ATGATGGAGTACTCGTTGGACGGACACAACGTGAG 634
GACCTTCCTGCGGCCGTACTACCAGACGGAGGAGGGCGAGGA 910
                                                                 GGCTGGCCTCCTGCGGAACCGCTGCTTCCTGGACAGTGCCTTTGTCAGGAACAACCA
                                                                                                                                       CGTCCTTCTGCTGTGCTTCTTCGTCTTCTTCATTTTCGGCATCGTTGGCGTCCAGCTCTG 808
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Snutch,T.P. and Baillie,D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32 from Patent W00102561. AX068907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuromed Technologies,
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:12578753
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RESULT 15
HSA420779
LOCUS
DEFINITION

HSA420779

Homo sapiens ${\tt mRNA}$ for calcium channel, voltage-dependent, alpha 1Hb subunit (CACNAlHB gene).

7044 bp

mRNA

linear

PRI 26-NOV-2001

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-NOV-2001) Jagannathan S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 7044)
Jagannathan, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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subunits in human male germ cells - expression of multiple
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AJ420779.1 GI:17129559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGSTSPORKGKNAGGPBOTGGHGFLESLNSPDBYEKI PHVAGEHGLGQARGHLSGLSVP
CPLPSPPAGTLTCELKSCPYCTRALEDPEGELSGSESGDSDGRGVYEFTQDVRHGDRW
DPTRPBRATDYPGGGEGOSPQRAQORAAPGEBGWMGRLWVTFSGKLTRI VDSKX FSRG
IMMAILVNTLSMGVEYHEQPEELTNALEISNIVFTSMFALEMLLKLLAGPLGYINP
YNIFDGIIVYLSYWEIVGQADGGLSVLÆTFRLLRVLKLVRFLPALRGUVVLVKTMDN
VATFCTLLMLFIFISILGMHLFGCKFSLKTDTGDTVPDRKNFDSLLMAIVTVEQILT
QEDWNNVLYNGMASTSSWAALIFVALMTFGNYVLFNLLVAILVEGFQAEGDANRSDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha 1HB subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEPGSCYEELLKYVGHIFRKVKRRSLRLYARWQSRWRKKVDPSAVQGQGPGHRQRRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NACINWNQYYNVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLEGWVDIMYYVMDAHS
FYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRARHLSNDSTLASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHVSMLVIMLNCVTLGMFRPCEDVECGSERCNILEAFDAFIFAFFAVEMVIKMVALGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                    HYLDLETTETICVNVITMSMEHYNQPKSLDEALKYCNYVFTIVEVEEAALKLVAFGER
REFKDRWNQLDLATVLLSLMGITLEETEMSAALPINPTIIRIKVLRTARVLKLLKMA
TGMRALLDTVVQALPQVGNLGLFMLLFETIAALGVELFGRLEGSEDNPCEGLSSHAT
TGMRALLDTVVQALPQVGNLGLFMLLFETIAALGVELFGRLEGSEDKPCEGLSSHAT
FYLYNGYFYTFVLVAQ
FYLYNVYYAVLMKHLEESNKEAREDAELDAEIELEMAQGPGSARRYDADRPPLPQESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDKTSVHFEEDFHKLRELQTTELKMCSLAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRGSSSSGDPPLGDQKPPASLRSSPCAPWGPSGAWSSRRSSWSSLGRAPSLKRRGQCGERESLLSGEGKGSTDDEAEDGRAAPGPAATPLRRAESLDPRPLRPAALPPTKCRDRDGQVVALPSDFFLKIDSHREDAAELDDDSEDSCCLRLHKVLEPYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHTASVHHLVYHHHHHHHHHYFSHGSPRRPGPEPGACDTRLVRAGAPPSPPSPGRGP
PDAESVHSIYHADCHIEGPQERARVAHAAATAAASLRLATGLGIMNYPTILPSGVGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYYQTEEGEENPFICSSRRDNGMQKCSHIPGRRELRMPCTLGWEAYTQPQAEGVGAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELGVSPSESPAAERGAELGADEEQRVPYPALAATVFFCLGQTTRPRSWCLRLVCNPWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLDSAFVRNNNLTFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGQKCYLGDTWNRLDFFIVVAGMMEYSLDGHNVSLSAIRTVRVLRPLRAINRVPSMRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental
/product="calcium_channel, voltage-dependent, T type,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="CACNA1HB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="CACNA1HB'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="germ cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'tissue_type="testes"
DAQGFLDKPGRADEQWRPSAELGSGEPGEAKAWGPEAEPALGARRKKKMSPPCISVEP
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                                                                                              VASVHSPPAESCASLQIPLAVSSPARSGEPLHALSPRGTARSPSLSRLLCRQEAVHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7044
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PAEDEGSARPSAAEGGSTTLRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWGQA
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PVGDPPEKRRGLYLTVPQCPLEKPGSPSATPAPGGGADDPV"
1209 a 2393 c 2216 g 1226 t
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BASE COUNT

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Matches 277;
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Best Local Similarity
                                                                                                                   1011 CATTGTGGCTCTTCCTGGAAACAGCAGCCTGGCCCCTGCCAATGGCTCGGCGCCCTGTGG 1070
                                              1071 GAGCTTCGAGCAGCTGGAGTACTGGGCCAACAACTTCGATGA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 ATGGTGGCCTTGGGGCTGTTCGGGCAGAAGTGTTACCTGGGTGACACGTGGAACAGGCTG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711
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                                                                                        756 GGCTGGCCTCCTGCGAACCGCTGCTTCCTGGACAGTGCCTTTGTCAGGAACAACAACCT 815
                                                                                                                                                                                  696 CGTCCTTCTGCTGCTTCTTCGTCTTCTTCATTTTCGGCATCGTTGGCGTCCAGCTCTG
                                                                                                                                                                                                                                                                             636 CGTGCCTAGCATGCGGATCCTGGTCACTCTGCTGCATACGCTGCCCATGCTCGGGAA 695
                                                                                                                                                                                                                                                                                                                                                                             582
                                                                                                                                                                                                                                                                                                                                                                                                     523 GATTTCTTCATCGTCGTGGCGGGC-ATGATGGAGTACTCGTTGGACGGACACAACGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            771 CTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGAC 830
                                                                                                                                                                                                                            951 GATCCTGGTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGCGT 1010
                                                                                                                                                                                                                                                                                                                         816 GACCTTCCTGCGGCCGTACTACCAGACGGAGGAGGGCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAAG 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCCTGGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGCGGCTCCGAGCG---CTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCATTTGCGTGTTCCTGGTGCTGGATGCAGATGTGCTGCTGCTGAGCGTGATGACTTC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTCTGCAACCCATGGTTCGAGCACGTGAGCATGCTGGTAATCATGCTCAACTGCGTG 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCTGGAGGCCTTTGACGCCTTCATTTTCGCCCTTTTTTGCGGTGGAGATGGTCATCAAG
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47.6%;
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Pred. No. 0.02;
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Search completed: October 8, 2002, 08:56:08
Job time: 2824 secs

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Database
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atgagctcagcctgctggga.....acctgtggctgtgcaggtga 1458
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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55.4	55.6	56	56.8	57.8	58.4	59	59.8	59.8	60.8	63.2	63.6	67.2	68	68.4	74.8	82	94.4	101.2	134.6	141.4	151.6	163.6	169.4	174	178.8	207.6	207.8
3.8				4.0		4.0		4.1	4.2	4.3	4.4	4.6	4.7	4.7	5.1	5.6	6.5		9.2	9.7	10.4	11.2	11.6	11.9	12.3	14.2	14.3
354	619	1049	441	579	643	622	844	663	833	159	545	341	394	461	507	383	580	631	691	579	178	852	434	338	596	673	262
12	12	9	10	10	9	10	10	9	10	9	10	9	10	12	10	10	9	9	9	9	10	10	9	10	10	9	9
FR0013559	FR0006820	AL550149	BF740717	BI682620	BB613655	BF513282	BG399273	AL133778	BI160381	AW867176	BF074505	AW321173	BI045473	AZ854774	BI855258	BF552166	AL528344	AV883460	AL632626	AW174364	BF330244	BI107285	AW178475	BF850563	BM231050	BB216125	AW177528
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ALIGNMENTS

FEATURES VERSION KEYWORDS REFERENCE SOURCE RESULT 1 BE141734/c DEFINITION ACCESSION LOCUS JOURNAL MEDLINE TITLE AUTHORS ORGANISM source Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-QVO-HT0101-061
099-032-h12&t3=1999-10-06&t4=1)
Seg primer: puc 18 forward
Seg primer: puc 18 forward l (bases 1 to 581)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jogeneel,C.V., O'Hare Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research Homo sapiens BE141734 581 bp mrNA linear EST 21-JUN-200 QVO-HT0101-061099-032-h12 HT0101 Homo sapiens cDNA, mRNA sequence. Tel: +55-11-2704922 Fax: +55-11-2707001 sequence tags Shotgun sequencing of the human transcriptome with ORF expressed Simpson, A.J. EST BE141734.1 GI:8604455 BE141734 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and quality sequence start: 26 quality sequence stop: 580 Natl. Acad. Sci. U.S.A. Location/Qualifiers /organism="Homo sapiens" 97 (7), 3491-3496 (2000) EST 21-JUN-2000

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BASE COUNT
ORIGIN
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AW177543/c
                                                         REFERENCE
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HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICE Human Cancer Genome Pr
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Unpublished (1999
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AGCATGAGCTCACAGATAG
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100999-001-B09&t3=1999-09-10&t4=1)
Seq primer: puc 18 forward
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nes 416; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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/clone_lib="Jurkat T-cells V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
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1 (bases 1 to 994)
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/lab_host="pH10B (TI phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

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Eutheria; Rodentia; Sciurognathi; Muridae;
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76.5%;
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE168889
QV1-HT0517-020400-148-g10
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                      Tel: +55-11-2704922
                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                            Contact: Simpson A.J.G.
                                                                                                                                                                                                                sequence tags
                                                                                                       Prof. Antonio
                                                     +55-11-2707001
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400-148-g10&t3=2000-04-02&t4=1)
              Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                         Homo sapiens
                                                                                   HCGP http://www.ludwig.org.br/ORESTES
The FAPESP/LICR Human Cancer Genome P
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Tel: +55-11-2704922
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This sequence was derived fro
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                                       TGGAGAACTTTCTTCACAAGTGGGACCGCCGCGGTCACCTAGAGCCTCTCGCGGGGGATT
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                                                                                                                    TTGTGCTGTGGTGGTGTCTGTCTGTCTGGGTCAACCTGTTTCTGGCTCTGATCC
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                                                                                                                                                                                                                                                                               ACAACTTCGACGACTTTGCTGCTGCCCTGGTCACTCTGTGGAACGTGATGGTTGTGAACA 177
                                                                                                                                                                                                                                                                                                                                                            TGGCCCCTGACAACGGCTCAGCACCCTGTGGGAGCTACGAGCAGCTGGAGTACTGGGCCA
                                                                                                                                                                                                ACTGGCAAGTCTTCCTGGATGCCTTCCAGCGCTTCGTGGGCCCGTGGTCGAAGATCTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, Estone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 104 row: A column: 19
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST discovery in swine 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI340329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /noter "Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." a 132 c 147 g 108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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Pred. No. 1.6e-64;
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Sus.
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 397
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                                                                                                                                                                                                                                                                                                   203 TGACTTCCCTCCTGGTGCTGCTGACCACGGCCAACAACCCCGATGTGATGATTCCTGCGT
                                        383 CTCTCCAGACCTCGCTGTTTCGGAGGCGGCTGGGAACCCGGGCTGCCTTTGAAGTCCTAT 442
                                                                                                                                                                                                                                                                                                                                                                                              Local
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 ATTCCAAGAACCGGGCCTATGCCATCTTCTTCATAGTCTTCACTGTGATAGGAAGCCTGT
                                                                           TTCTGATGAACCTGCTGACAGCCATCATCTACAGTCAGTTCCGGGGGCTACCTGATGAAAT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10610 row: j column: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage=resistant);
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: Not1;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 295 c 318 g 249 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE: 4752492"
/clone_lib="NCI_CGAP_Skn4"
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92.0%;
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Pred. No. 5.8e-62;
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IMAGE:4752492 5',
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TITLE
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  656 GGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAAGGTCTT
                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                         CGGCCACTACTTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTGTCCAT 595
                                         TTGCGTGTTCCTGGTGCTGGATGCAGATGTGCTGCTGCTGAGCGTGATGACTTCATCCT 655
                                                                                                                                                                                                                                                                                                311;
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BM049977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                             /Clone_lib="NH_MCC_40"
/Clone_lib="NH_MCC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DHHOB (phage-resistant)"
/lab_host="DHHOB (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: xhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAGG). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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cDNA clone IMAGE:5450134 5',
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                         476 AGGCCACCCGAGGCCCGAGTACCAGTCTCCGTTTCTGCAGAGCGCCCAGTTCCTCTT 535
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               72
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AGAGCACCCGCCGAGGCCCGAGTACCAGTCTCCGTTTCTGCAGAGCGCCCAGTTCCTCTT 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESD/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-RC6-ST0198-081
199-021-A12&t3-1999-11-08&t4-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dias Neto, E.,
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                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence start: 11 quality sequence stop: 349
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                          /note-*Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                    tissue mRNA and cDNA amplification were performed under low stringency conditions."
102 c 92 g 94 t
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                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="ST0198"
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                       Score 275.8; DB 9
                                                                                        Mismatches
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
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Ludwlg Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
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n quality sequence stop:
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         // note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CT0159"
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Local Similarity

18.6%;

Score 270.8; DB Pred. No. 2e-49; Mismatches

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1 (bases 1 to 922)
NIH-MGC http://mr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10367 row: k column: 14
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tlssue_type="retina"
/tlssue_type="retina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGCGTCATTGTGGCTCTTCCTG 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 396)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL528343 LTI_NFL003_NBC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                  BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
/note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
                                                                                                                                                                          /tissue_type="neuroblastoma cells"
/lab_host="DH108"
                                                                                                                                                                                                                                                              /clone="CSODC023YP19"
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                        /clone_lib="LTI_NFL003_NBC3"
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AV668288
                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
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Establishment of a high throughput EST sequencing system using ESTAPLISHMENT OF A high throughput EST sequencing system using EstaPlishment of a high throughput EST sequencing system using EstaPlishment of 36,000 period of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kazusugi@cocoa.ocn.ne.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshikazu Sugimoto
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21570554
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               /note="Vector: pZL1; Site_1: ;
was deleted from a Not1 site"
112 c 127 g 75 t
                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E10V020H12"
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http://fulllength.invitrogen.com"
a 103 c 113 g 69 t 7 ot
                                                                                                                                      /tissue_type="ovary"
/dev_stage="fetus"
                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                             /clone_lib="Bos taurus ovary
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Pred. No. 1.4e-48;
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Best Local Sim
Matches 315;
                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGCTGTGGGACATGACGCGGCTCGTGAACGTGCTCATCGTCTTCCGCTTCCTGCGCATC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTGTTCGACGGGCTCCTCACCATCGTCCTGCTGGAAGCCGGCGACGCTGGGCCTGCTG
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                                                                                                                 FORWARD: AGGADACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 94 row: O column: 17
                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                    Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                   Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                    PCR PRimers
                                                                                                                                                                                                  Single pass sequencing. Bases ov v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG385307
BG385307.1
                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                         and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                         Stone, R.T., Heaton, M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 489)
Fahrenkrug, S.C., Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
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306972 MARC 1PIG Sus scrofa
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              /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
                                                                               Location/Qualifiers
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Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 267.2; DB 9
Pred. No. 1.5e-48;
0; Mismatches 59
pooled'
                                                                                                                                                                                                                                                                                    NE 68933-0166, USA
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                                                                                                                                                                                                  called and alt_trimmed with phred by cross_match with the -minscore 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Sus.
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Search completed: October 8, 2002, 09:08:36 Job time: 1624 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.2%; Score 250.4; DB 10; Length 489; Best Local Similarity 85.8%; Pred. No. 7.7e-45; Matches 278; Conservative 0; Mismatches 46; Indels 0; Gaps
                                                               122 GGAGCTGCCGCTTCTGCTCTCAGCAGGATGATGGGCAGGACAGGGAGAGGCTGACCTACT 181
                                                                                                                                                                                                                                                                          286 CTGATGTGATGCTGCGTATTCCAAGAACCGAGCCTACGCCATCTTCTTCATAGCCT 345
                                                                                                                                                                                                                                                                                            242 CCGATGTGATGATTCCTGCGTATTCCAAGAACCGGGCCTATGCCATCTTCTTCATAGTCT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=""Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
88 a 151 c 133 g 117 t
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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577.4
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253.2
                                                                                                                                                                                                                                                                                                                                         Score
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1458
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Gapop 10.0 , Gapext 1.0
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      73.6
61.0
55.5
51.6
39.6
39.6
33.2
22.2
17.4
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4: \SIDSI_gcgdata/hold-geneseq_geneseqn-embl_NA1983.DAT: *
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5: \SIDSI_gcgdata/hold-geneseq_geneseqn-embl_NA1985.DAT: *
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					pic; immunosuppressant; cytostatic; gene revous system; neuropathy; central nervous Parkinson's disease; Huntington's disease, ateral sclerosis; Shy-Drager Syndrome; ch thrombolytic; drug screening; arthritis;	NO 376.			6 Bp.	ALIGNMENTS	AAX83486 AAX83487 AAX83487 AAZ52309	ABAU8302 AAX83488	AAS16827	AAF31678	AAT / 0228 AAZ 58941	AAT96811	AAN91778	AAX59083 AAX83491	AAK74093	AAZ32162	AAQ25388	AAI58060 .	AAF27717	AAH98560	AAF55042	AAF55046	AAX59080 AAX59081	AAX59082	AAX83490	AAA00547 AAF31682
					;; gene therapy; cancer nervous system; CNS; disease; haemostatic; come; chemotactic; hritis; inflammation;						Rat T-type voltage Rat T-type voltage Rat T-type voltage Rat pancreatic T-	an Ca ch T-type	Human T-type calc	Rat alpha-IH calci	Rabbit calcium Rabbit skeleta		seleta	Human activated ca Human T-type volta	=	Human endothelial	TXA2 receptor	Human 10n channel Human polynucleoti	Human transport	Rat EST-derived	Human colon cancer Nucleotide sequenc	otide:		Human T-type voita	т-tуре	Human colon cancer Human alpha-IH cal

human polynu

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CC The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, CC immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous cystem, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, arthritis and inflammation, leukaemias and CC c.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed CC specification.
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CC The present sequence encoding for human TANGO 437 is isolated from cDNA CC clone jthha045b02 from a human mixed lymphocyte reaction cDNA library. CC TANGO 437 is 1 of 4 novel human transmembrane proteins which also CC includes TANGO 315 (AAU00498-AAU00499), TANGO 330 (AAU00500-AAU00501) CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins CC are useful as modulating agents in regulating a variety of cellular CC processes and can be used to express the proteins in a host cell in CC gene therapy applications. Antisense nucleic acid molecules and CC expression vectors containing the TANGO nucleic acids are also described. CC Diagnostic assays can be used to detect genetic alterations in the TANGO nucleic acids and to identify compounds that bind to or modulate activity CC monitor protein levels in tissue as a clinical testing procedure. CC TANGO 437 shows homology to human Gene 100. TANGO 437 nucleic acids acids acids acids conditions and proteins may be used to diagnose, treat and monitor immune-related CC cell proliferative disorders (e.g. lymphoma, cancer) and autoimmune CC disorders e.g. arthritis
   Query Match
Best Local Similarity
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} 
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DB; AAU00502.
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/product= "TANGO 437 protein"
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       61.0%;
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       1.4e-210;
                                       DB 22;
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                          TTGGCGGGATCCTGGT-----
                                                               CCCTGGCAAACCTGGTGTCCATTTGCGTGTTCCTGGTGCTGGATGCAGATGTGCTGCCTG
TIGGCGGGATCCIGGGGACCACIGGGGTGAGAAGGTGTCTCIGGGGCIGCAGGGTGCT 1846
                                                  TGTACCGATTGCCACACCCAGGCTGGAGGCCGGAGATGGTGGGCCTGCTGTGTGGG
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                                                                                                                                                                                                                                                      TGGAGATGCTGCTCAAGGTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCA
                                                                                                                                                                                                                                                                                                         CTGAGCGTGATGACTTCATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGT
                                                                                                                                                                                                                                                                                                                                                          CCCTGGCAAACCTGGTGTCCATTTGCGTGTTCCTGGTGCTGGATGCAGATGTGCTGCCTG
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                                                                                                                                                Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allery; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid, digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1430
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                                                                                                                                                                                                                                                                                                                                                            AAV59758
                                                                                                                                                                                                                                                                    Human secreted protein gene 100 clone HEONN58.
                                                                                                                                                                                                                                                                                                   19-JAN-1999
                    06-MAR-1998;
                                                 11-SEP-1998
                                                                              WO9839448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCACTCTGTGGAACTTGATGGTGGTGAACAACTGGCAGGTGTTTCTGGATGCATATCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                       metabolism; regulation;
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                     98WO-US04493.
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                                                                                                                                       malabsorption; gastritis; neoplasm
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          11-APR 1997
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
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         11-APR-1997
11-APR-1997
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23-MAY
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07-MAR-1997;
11-APR-1997;
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970S-004311

970S-0043312

970S-0043568

970S-0043568

970S-0043578

970S-0043578

970S-0043672

970S-0047501

970S-0047501

970S-0047502

970S-0047503

970S-0047583

970S-0047583

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970S-0047586

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97US-0038621.
97US-0040161.
                                                                                 s-0056636.
s-0056637.
s-0056662.
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                                                                                                                                                                                                                             This sequence represents a nucleic acid molecule designated Gene 100 from the human cDNA clone HEONN58 (deposited as clone ATCC 97897 and ATCC 209043) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAV74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides specific uses are described for each of the 186 column of the second column of the new polynucleotides, based on which tissues they are most highly expressed in read analysatil for Asserting medical in the second column of the new polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                Matches
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Kyaw H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1997
23-AUG-1997
24-AUG-1997
25-AUG-1997
26-SEP-1997
27-AUG-1997
28-AUG-1997
29-AUG-1997
29-AUG-1997
29-AUG-1997
20-SEP-1997
20-SEP-1997
20-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                          Sequence 2377 BP; 462 A; 671 C; 650
                                       535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bednarik DP,
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22-AUG-1997
TCGGCCACTNACTTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTGTCC
                  TCGGCCACT-ACTACTTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTGTCC 593
                                                                               AGGCCACCCGCCGAGGCCCCGAGTACCAGTCTCCCGTTTCTGCAGAGGCG-CCCAGTTCCTCT 534
                                                             1998-506364/43.
                                                                                                                                                                                                                        AAV59511 for described uses).
                                                                                                                                  957;
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                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW74973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP, Brewer LA, Carter KC, Duan R, Ebner R, Ferrie AM, Fischer CL, Florence KA, Greene J Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z
                                                                                                                                  Conservative
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970S-0056908.
970S-0056909.
970S-0056910.
970S-0057651.
970S-0057650.
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970S-0057761.
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91.7%;
                                                                                                                             Pred. No. 9.807; Mismatches
                                                                                                                                            Score 809.4;
Pred. No. 9.8
                                                                                                                                                                                          G;
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                                                                                                                                            9.8e-191;
                                                                                                                                                         DB 19; Length
                                                                                                                                                                                         T; 16 other;
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cDNA; 1734

12-OCT-2001 AAH99106;

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                                                                              CACCTGCAGCCCCTTGCTGGGACCCCAGAGGCCACCTACCAGATGACTGTGGAGCTCCTG
                    CCGCACCTGTGGCTGTGCAGGTGA 1458
                                                  CCGCACCTGTGGCTGCAGGTGA 1562
                                        TTCAGGGATATTCTGGAGGAGCCCGGGGAGGATGAGCTCACAGAGAGGCCTGAGCCAGCAC
                                                                                                                          CTGTGGAACTTGATGGTGGTGAACAACTGGCAGGTGTTTCTGGATGCATATCGGCGCTAC
                                                                                                                                                                                                                         CTGTGGAACTTGATGGTGAACAACTGGCAGGTGTTTCTGGATGCATATCGGCGCTAC
                                                                                                                                                                                                                                                      {\tt TTCGAGCAGCTGGAGTACTGGGCCAACAACTTCGATGACTTTGCGGCTGCCCTGGTCACT}
                                                                                                                                                                                                                                                                   TTCGAGCAGCTGGAGTACTGGGCCAACAACTTCGATGACTTTGCGGCTGCCCTGGTCACT
                                                                                                                                                                                                                                                                                                GTGGCTCTTCCTGGAAACAGCAGCCTGGCCCCTGCCAATAGGTCGGCGCCCTGTGGGAGC
                                                                                                                                                                                                                                                                                                             GTGGCTCTTCCTGGAAACAGCAGCCTGGCCCCTGCCAATGGCTCGGCGCCCCTGTGGGAGC
                                                                                                                                                                                                                                                                                                                                          CTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGCGTCATT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000; 2000US-0491404
17-JUL-2000; 2000US-0617746
03-AUG-2000; 2000US-0631451
15-SEP-2000; 2000US-0663870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostics; forensic test; gene mapping; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 756-757; 1275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tomato; monkey;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1734 BP; 315 A; 451 C; 531 G; 436 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                  of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
  1064 CCTGTGGGAGCTTCGAGCAGCTGGAGTACTGGGCCAACAACTTCGATGACTTTGCGGCTG
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                                                                                                                                                                                                                          CGGGCTCCTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGG
                                                                                                                           GCTCAAGGTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-476164/51.
DB; AAM24447.
                            GCTCAAGGTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGA
                                                                                        TTGGCGGGATCCTGGTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTA
                                                                                                                                                                            ACATGACCCGCATGCTGAACATGCTCATCGTGTTCCGCCTTCCTGCGTATCATCCCCAGCA
                                                                             TTGGCGGGATCCTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST-derived coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                             753;
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                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cow; fruit fly; yeast; hamster; macaque; horse;
g; sea urchin; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                       51.6%;
99.7%;
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Pred. No. 1.2
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nan T;
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RESULT 5
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11-APR-1997;
11-APR-1997;
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
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                                                                                                                                                                                                                                                                07-MAR-1997;
07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
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05-SEP-1997;
05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed (see AAV59511 for described uses).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                                                                                                                                                                                                                                                          AGCATGAAGCCGATGGCCGTGGTGGCCAGTACCGTCCTGGGCCTGGTGCAGAACATGCGT 939
                           GCGTTTGGCGGGATCCTGGTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTG 999
GCTGCCCTGGTCACTCTGTGGAACTTGATGGTGGTGAACAACTGGCAGGTGTTTCTGGAT
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                                                                                        GCTGCCCTGGTCACTCTGTGGAACTTGATGGTGGTGAACAACTGGCAGGTGTTTCTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents a nucleic acid molecule designated Gene 101 the human cDNA clone HLQAB52 (deposited as clone ATCC 97901 and 209047) which encodes a secreted human protein. The gene can be
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Ferrie AM, Fis
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99.8%;
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Fischer CL, Florence KA, Greene JM, Hu J
, Li Y, Moore PA, Ni J, Olsen HS, Rosen
Soppet DR, Young PE, Yu GL, Zeng Z;
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25-APR-2000;
09-JUL-2000;
           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
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Zhou P,
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Wehrman T,
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                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for system injuries -
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assays for receptor activity, arthritis and C.N.S disorders.
Note: The sequence data for this natural aid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 966 BP; 170 A; 276 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 AACCTGCCTGAGTCTCTGACTTCCCTCCTGGTGCTGACCACGGCCCAACAACCCCCGAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
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                                     789
                                                                                                                                           669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGATGATTCCTGCGTATTCCAAGAACCGGGCCTATGCCATCTTCTTCATAGTCTTCACT 306
                                                                                                                                        ATTGTGTACTACCTGTTGGAGTTGCTGCTCAAGGTCTTTGCCCTGGGCCTGCGAGGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTACCTGATGAAATCTCTCCAGACCTCGCTGTTTTCGGAGGCGGCTGGGAACCCGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGATGTGCTGCCTGAGCGTGATGACTTCATCCTGGGGATTCTCAACTGCGTCTTC
                                                                                                                                                                                                                                                              CTGGGGAACCTCATCGCCCTGGCAAACCTGGTGTCCATTTGCGTGTTCCTGGTGCTGGAT
                                                                                                                                                                                                                                                                                                   TACCAGTCTCCGTTTCTGCAGAGCGCCCAGTTCCTCTTCGGCCACTACTACTTTGACTAC
                                                                                                                                                                                                                                                                                                                TACCAGTCTCCGTTTCTGCAGAGCGCCCAGTTCCTCTTCGGCCACTACTACTTTGACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAAGCCCCAGAACTTGCTGCAGGTGCTTCAGAAGGTCCAGCTGGACAGCTCCCACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTACCTGATGAAATCTCTCCAGACCTCGCTGTTTCGGAGGCGGCTGGGAACCCGGGCT
CTGCTGTCGCTGTGGGACATGACCCGCATGCTGAACATGCTCATCGTGTTCCGCTTCCTG
                                   ATCTCAACTCTGGCTGTGTACCGATTGCCACACCCAGGCTGGAGGCCGGAGATGGTGGGC
                                                                                        CTGTCCTACCCCAGCAACGTGTTTGACGGGCTCCTCACCGTTGTCCT--------
                                                                                                                                                                                              GCAGATGTGCTGCCTGAGCGTGATGACTTCATCCTGGGGATTCTCAACTGCGTCTTC
                                                                                                                                                                                                                                                  CTGGGGGAACCTCATCGCCCTGGCAAACCTGGTGTCCATTTGCGTGTTCCTGGTGCTGGAT
                                                                                                                                                                                                                                                                                                                                                        CAGAAGCTCTTCAACGAGCTTGACAGAAGTGTGGTTAAAGAGCACCCGCCGAGGCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                   -----CACCGCGAGGCCCGAG
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Pred. No.
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                                                 -----GCTGGAGGCCGGAGATGGTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and therapy, drug screening, inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 219;
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RESULT 7
AAH16386
ID AAH1
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         Best Loc
Matches
                                            Query Match
                                                                                                           sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers ets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-off primer and an oligonucleotide complementary to the complementary strand of a polyuucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polyuucleotide which comprises a 5'-end sequence complementary to the component of a polyuucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8;
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-01187676.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH16386 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000;
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         Local Similarity
les 326; Conserv
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                                                                            2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID 15338; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugiyama
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                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; diagnosis; antisense therapy; gene therapy;
                                                                          383 A; 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa T,
                        22.2%;
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Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2200 BP
                                     Score 324.2;
                                                                        C; 671 G; 511
1.8e-70;
3;
                                     DB 22;
                                                                        T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K,
(, Otsuki
                                     Length 2200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection
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Conservative

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Mismatches

Indels

0;

Gaps

0;

AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed

Claim 1;

Page 792; 1097pp; English.

Pred. No.

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CCCCCXX
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AAA02076
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Lamson G, Drugshire
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
                                                                                                                                                      Polynucleotide library used to
                                                                                                                                                                                                      WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
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                                                                                                                                                                                                                                                  Leshkowitz D,
                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON
(HYSE-) HYSEQ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer cell line polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA02076 standard; cDNA; 991 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCACCCGCACCTGTGGCTGTGCAGGTGA 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTACTCAGGCCCGTGGTCCAAGATCTATTTTGTATTGTGGTGGCTGGTGTGTCGTCTGTCA
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                                                                                                                                                                                                                                                                                                                     Escobedo
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98US-0085537.
98US-0085696.
98US-0105234.
98US-0105877.
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                                                                                                                                                                                                                                                                     Randazzo F, K
Crkvenjakov R,
                                                                                                                                                                                                                                                  Garcia
                                                                                                                                                                                                                                               Innis MA, Garcellinais MA, Garcellinais MA, Garcellinais MA, Partie Market Mark
                                                                                                                                                      determine
                                                                                                                                                                                                                                                                          Garcia PD, successive GC, Pot D,
                                                                                                                                                      cancerous
                                                                                                                                                                                                                                               Stache-Crain
                                                                                                                                                                                                                                                                                                                Sudduth-Klinger J;
                                                                                                                                                      states
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                                                                                                                                                                                                                                                                                        Kassam
                                                                                                                                                      of mammalian
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                                                                                                                                                                                                                                                                     Labat
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RESULT 9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastratic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, cestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 991 BP; 127 A; 207 C; 225 G; 265 T; 167 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          negative breast cancer, lung cancer, and colon cancer.
              09-APR-2001
                                                                AAF66352;
                                                                                                         AAF66352 standard; cDNA; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 TCTGCAGAGCGCCCAGTTCCTCTTCGGCCACTACTACTTGACTACCTGGGGAACCTCAT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 TGTGTACCGATTGCCACACCCAGGCTGGAGGCCCGGAGATGGTGGGCCCTGCTGTCGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 TGCTGAGCGTGATGACTTCATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 CGCCCTGGCAAACCTGGTGTCCATTTGCGTGTTCCTGGTGCTGGATGCAGATGTGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 TNCCCCTCCCNNNCNNNTNTNNNNNNNNNTNAGTTNACAGTAGGANGNGGAGGCTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THACGTGTNGGGACHNICATCCTGGGGCATTHTCAACTGCGTHTCATTGTGTACTHTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGAAGCCGATGGCCGTGGTGGCCAGTA-CCGTCCTGGGCCT-GGTGCAGAACATGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGGAGATGCTGCTCAAGGTCTTNGGCCTGGTCCTGCGAGGGTACCTGTCCTACCCCAG
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                                                                                                                                                                                                                                                                   ATGGCTCGGCGCCC--TGTGGGAGCTTCGAGCAGCTGGAGTACTGGGCCAACAA 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACATGACCCGCATGCTGAACATGCTCATCGTGTTCCGCCTTCCTGCGTATCATCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACGTGTTTGACGGGCTCCTCACCGTTGTCCTGCTGGTTTTGGAGATCTCAACTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACGTGTTTGACGGGCTCCTCACCGTTGTCCT-------
                                                                                                                                                                                                                                                                                                                                           ACTT--GTTTAGAGGCGTCATTGTGGCTCTTCCTGGAAAC-AGCAGCCTGGCCCCTGCCA 1051
                                                                                                                                                                                                                                                                                                                                                                                                              TGCTTTTTGGCCGGGATCCTGGTGGTNGGTCTACTACGTATTTGCCATCATTTGGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACATGACCCGCATGCTGAACATGCTCATCGTGTTCCGCTTCCTGCGTATCATCCCCAG
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                                                                                                                                                                                                                          ATGGCTNGGCGCCCCTGTGGGANCTTTNCAGCAGCTGGANTACTTGGGGCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGTTT----GGCGGGATCCTGGTGGT-GGTCTACTACGTATTTGCCATCA-TTGGGATCA
                                                                                                                                                                                                                                                                                                                   ACTTTGTTTTAGAGGCGTNATTGTGGCTCTTCCTGGAAACAAGCATCCTGGCCCCTGCCA
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                   (first entry)
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Pred. No. 5.6
                                                                                                              ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
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Best Local :
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams LT,
Reinhard C, F
Crkenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast cancer; lung cancer; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polynucleotide, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-091805/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 850; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000WO-US18374.
                                                                                                                                                                                                                                                                                                                   Sequence 381 BP; 75 A; 121 C; 94 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                               dysplasia and
                                                                                                                                                                                                                                                                                                                                                             treat the cancers and proliferative disorders such as neoplasia,
                                                        316
                                                                                                                                                                                                                 184
                                                                                      124
                                                                                                                 256
                                                                                                                                                                         196
                                                                                                                                               64
                                                                                                                                                                                                     4
ATGAAATCTCTCCAGACCTCGCTGTTTCGGAGGCCGGCTGGGAACCCCGGGCTGCCTTTGAA 435
                                                                                   GAGTCTCTGACTTCCCTCCTGGTGCTGCTGACCACGGCCAACAACCCCGATGTGATGATT
                                                                                                                                                                                                    TGCTGTCGGCAGGATGATGGGCAGGACAGGGAGAGGCTGACCTACTTCCAGAACCTGCCT
                               359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; gene therapy; colon cancer; prostate cancer;
                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Randazzo F,
R, Drmanac S,
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                            hyperplasia.
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99US-0142311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones
                                                                                                                                                                                                                                                                            16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kennedy GC,
Dickson M,
LW, Strache-
                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                            Score 242; DB 22;
Pred. No. 2.4e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is MA, Garcia PD, Klinger J, Kassam
edy GC, Pot D, Lamson G, Drmanac R;
kson M, Labat I, Leshkowitiz D;
Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IJ
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                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                         Length 381;
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                                                                                 AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or
                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                         cells
                                                                                                                                                                                                                                                                                                   WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                             Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1999
                                                                                                                                                                                                                                                                     Polynucleotide library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer; tumour; diagnosis; gene expression product;
                                                                                                                                                                                                                          Page 308;
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                                                                                                                                                                                                                                                                                                                                                                         Escobedo
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98US-0105234.
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98US-0085537
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                                                                                                                                                                                                                       1097pp; English.
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                                                                                                                                                                                                                                                                  used to determine cancerous states of
                                                                                                                                                                                                                                                                                                                                           J, Innis MA, Garcia PD, Sudduth-Klinger
Randazzo F, Kennedy GC, Pot D, Kassam A,
Crkvenjakov R, Dickson M, Drmanac S, Lak
                                                                                                                                                                                                                                                                                                                              Garcia V,
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                                                                                                                                                                                                                                                                                                                              Stache-Crain
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                                                                                                                                                                                                                                                                  mammalian
                                                                                                                                                                                                                                                                                                                                           Labat
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                                                                                            Novel T-type calcium channel alpha-1 subunit gene useful for treating cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder
                                                                                                                                                                                                                                                                                                                                               Human; expressed sequence tag; EST; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic; T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor negative breast cancer, lung cancer, and colon cancer.
                                                                                                                                  P-PSDB;
                                                                                                                                                                    Snutch TP,
                                                                                                                                                                                                                  02-JUL-1999;
                                                                                                                                                                                                                                         04-JUL-2000;
                                                                                                                                                                                                                                                                 11-JAN-2001
                                                                                                                                                                                                                                                                                         WO200102561-A2
                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                        epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF31682 standard; cDNA; 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 300
                                                                                                                                                                                            (NEUR-) NEUROMED TECHNOLOGIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGTTGGAGTTGCTGCTCAAGGTCTTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249;
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                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                          2000WO-CA00794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 44 A; 88 C; 85 G; 83 T; 0 other;
                                                                                                                                                                                                                  99US-0346794
                                                                                                                                                                                                                                                                                                                                                                                                   calcium
                                                                                                                                                                                                                                                                                                                                        calcium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                   channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 188.4; DB 2
Pred. No. 4.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCT
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The present sequence is given in a specification providing secand partial sequences for three types of mammalian (human and T-type calcium channel subunits. An expression cassette has be generated which comprises a nucleotide sequence encoding a T-t

sequence encoding a T-type

Example 1; and epilepsy

Page

98-99;

103pp;

English.

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AAX83490
ID AAX83
XX AX83
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XY Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1608 BP; 261 A; 528
                                                                                                      WO9929847-A1
                                                                                                                                                                                                                                  activation;
                                                                                                                                                                                                                                                                                                                                  Human T-type voltage-gated Ca channel alpha-1-H (hCavT2b) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX83490 standard; cDNA; 6114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1071 GAGCTTCGAGCAGCTGGAGTACTGGGCCAACAACTTCGATGA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1011 CATTGTGGCTCTTCCTGGAAACAGCAGCCTGGCCCTGCCAATGGCTCGGCGCCCTGTGG
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         711 GTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGACGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522 G;
                                                                                                                                                                                                                                  drug;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-H designated hCaVT2b.

Voltage-gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics and slow activation fast inactivation kinetics and slow tail current. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6114 BP; 1056 A; 2047 C; 1894 G; 1117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New T-type voltage-gated calcium channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LOYO ) UNIV LOYOLA CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to treat cardiomyopathy, epilepsy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 CTCTTCGGCCACTACTTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTG
                                                                                                                                                                              579
                                                                                                                                                                                                                                                                   520
                                                                                                                                                                                                                                                                                                                                                         460
                                                                                                                                                                                                                                                                                                                                                                                                   711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 TCCATTTGCGTGTTCCTGGTGCTGGATGCAGATGTGCTGCCTGAGCGTGATGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                               GATCCTGGTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGCGT
                                                                                     CGTGCCTAGCATGCGGATCCTGGTCACTCTGCTGCTGGATACGCTGCCCATGCTCGGGAA
                                                                                                                                                                                                                       CCGCATGCTGAACATGCTCATCGTGTTCCGCCTTCCTGCGTATCATCCCCAGCATGAAGCC
                                                                                                                                                                                                                                                                   GATTTCTTCATCGTCGTGGCGGGC-ATGATGGAGTACTCGTTGGACGGACACAACGTGAG
                                                                                                                                                                                                                                                                                                             CTCACCGTTGTCCTGCAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGAC
                                                                                                                                                                                                                                                                                                                                                                                                   GTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGACGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCCTGGAGGCCTTTGACGCCTTCATTTTCGCCTTTTTTGCGGTGGAGATGGTCATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAAG
CGTCCTTCTGCTGTGTTCTTCGTCTTCTTCATTTTCGGCATCGTTGGCGTCCAGCTCTG
                                                                                                                                                                           CCTCTCGGCTATCAGGACCG-----TGCGGGTGCTGCGGCCCCTCCGCGCCATCAACCG
                                                                                                                                                                                                                                                                                                                                                         ATGGTGGCCTTGGGGCTGTTCGGGCAGAAGTGTTACCTGGGTGACACGTGGAACAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCTGGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGCGGCTCCGAGCG---CTGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US23161
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Pred. No. 8.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6114;
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1011 CATTGTGGCTCTTCCTGGAAACAGCAGCCTGGCCCCTGCCAATGGCTCGGCGCCCTGTGG

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RESULT 13
AAX83489
ID AAX83
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                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 103-111; 138pp; English.
                                                                                                                                                                                                                Sequence 6132 BP;
                                                                                                                                                                                                                                                  to treat cardiomyopathy, epilepsy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New T-type voltage-gated calcium channels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human T-type voltage-gated Ca channel alpha-1-H (hCavT2a) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX83489 standard; cDNA; 6132
531 CTCTTCGGCCACTACTTCGACTACCTGGGGGAACCTCATCGCCCTGGCAAACCTGGTG 590
                                                                                                                                                           POCGI
                                                     CTGGTCTGCAACCCATGGTTCGAGCACGTGAGCATGCTGGTAATCATGCTCAACTGCGTG 342
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                                                                                                                                                         Similarity
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                          1059 A; 2055 C; 1899 G; 1119 T; 0 other;
                                                                                                                                                     4.18;
                                                                                                                                                 Score 60; DB 20;
Pred. No. 8.4e-05;
                                                                                                                             Pred. No. 8.4e
0; Mismatches
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                                                                                                                                     295;
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               P-PSDB; AAY06300
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CDS
                                   WPI; 1999-371096/31
                                                                         Williams
                                                                                                                                                                   10-NOV-1998;
03-DEC-1997;
                                                                                                                                                                                                                          03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     endocrinological disorder; cardiovascular disorder; urological disorder; hepatic disorder; respiratory vascular disorder; ds.
                                                                                           Hans M,
                                                                                                                               (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                10-JUN-1999
                                                                                                                                                                                                                                                                                                  WO9928342-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium channel subunit 1H-2; human; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human activated calcium channel alpha 1H-2 subunit cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 GTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGACGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCACCGTTGTCCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGAC
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                                                                       3
                                                                                       Harpold M,
                                                                                                                                                                   98US-0188932
97US-0984709
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the nucleotide sequence of cDNA coding for the alpha 1H-2 subunit (see AAY06300) of a human low-voltage activated calcium channel. The cDNA was obtained by PCR amplification from a TT cell cDNA library. The invention provides calcium channel subunits, and isoform alpha 1H-2. The 1H-2 isoform contains a 957 nucleotide deletion relative to alpha 1H-1, resulting in a loss of 319 amino acids within the intracellular loop between domains II and III. The splice variant deletion was identified by PCR in all cells and tissues examined. These included TT cells, amyddala, caudate nucleus, putamen, heart, kidney and liver cells. Cells and vectors containing these nucleic acids, and methods for identifying containing these nucleic acids, and methods for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6941 BP; 1146 A; 2333 C; 2225 G; 1237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compounds that modulate the activity of calcium channels that contain these subunits are provided by the invention. Such compounds are used to treat calcium channel mediated disorders including neurological, endocrinological, cardiovascular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1(c); Page 162-171; 171pp;
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                     AAX59080 standard; cDNA; 7898
                                                                                                   1064 GACCTTCCTGCGGCCGTACTACCAGACGGAGGAGGGCGAGGA 1105
                                                                                                                                   1071 GAGCTTCGAGCAGCTGGAGTACTGGGCCCAACAACTTCGATGA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534 CTGGTCTGCAACCCATGGTTCGAGCACGTGAGCATGCTGGTAATCATGCTCAACTGCGTG 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 CTCTTCGGCCACTACTACTTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTG 590
                                                                                                                                                                                                                                                                                                                                                                                                                               771 GATTTCTTCATCGTCGTGGCGGGC-ATGATGGAGTACTCGTTGGACGGACACAACGTGAG
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                                                                                                                                                                                                 CATTGTGGCTCTTCCTGGAAACAGCAGCCTGGCCCTGCCCAATGGCTCGGCGCCCTGTGG
                                                                                                                                                                                                                                   CGTCCTTCTGCTGTGCTTCTTCGTCTTCTTCATTTTCGGCATCGTTGGCGTCCAGCTCTG
                                                                                                                                                                                                                                                                                                                               ACCCTGGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGCGGCTCCGAGCG----CTGCAAC
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                                                                                                                                                                   GGCTGGCCTCCTGCGGAACCGCTGCTTCCTGGACAGTGCCTTTGTCAGGAACAACAACCT 1063
                                                                                                                                                                                                                                                                 GATCCTGGTGGTGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGCGT 1010
                                                                                                                                                                                                                                                                                                 CGTGCCTAGCATGCGGATCCTGGTCACTCTGCTGCTGGATACGCTGCCCATGCTCGGGAA 943
                                                                                                                                                                                                                                                                                                                                                                                               CCGCATGCTGAACATGCTCATCGTGTTCCGCCTTCCTGCGTATCATCCCCCAGCATGAAGCC 890
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                                                                                                                                                                                                                                                                                                                                                               CCTCTCGGCTATCAGGACCG-----TGCGGGTGCTGCGGCCCCTCCGCGCCATCAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCTGGAGGCCTTGACGCCTTCATTTTCGCCTTTTTTGCGGTGGAGATGGTCATCAAG 710
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47.68;
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03-DEC-1997;
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                                                                                                                                                       534
                                                                                                                     TCCATTTGCGTGTTCCTGGTGCTGGATGCAGATGTGCTGCCTGAGCGTGATGACTTC 650
                         ATCCTGGAGGCCTTTGACGCCTTCATTTTCGCCTTTTTTTGCGGTGGAGATGGTCATCAAG
                                                       ATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAAG
                                                                                       ACCCTGGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGCGGCTCCGAGCG---CTGCAAC 650
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channel. This full-length cDNA sequence was deduced from coverlapping partial clones isolated from a Tr cell cDNA library. Overlapping partial clones isolated from a Tr cell cDNA library. The invention provides calcium channel subunits, including 2 splice wariants of alpha 1H-1 (see also AAX59081), and isoform alpha 1H-2 (see AAX59082). The 1H-1 splice variants were detected by RT-PCR in multiple tissues. They differ only at codon 2230, being either GAC (Asp) or GAA (Glu). 1H-2 has a 957 nucleotide deletion in the I-II intracellular loop when compared with 1H-1. Cells and vectors containing these nucleic acids, and methods for identifying compounds that modulate the activity of calcium channels that compounds are used to treat calcium channel mediated disorders, and methods are used to treat calcium channel mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium channel subunit 1H-1; human; neurological disorder; endocrinological disorder; cardiovascular disorder; urological disorder; hepatic disorder; respiratory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of cDNA coding for the alpha 1H-1 subunit (see AAY06298) of a human low-voltage activated calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vascular disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1(c); Page 138-149; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subunits of calcium channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-371096/31
                                                                                                                                                                                                                                                                                                Sequence 7898 BP; 1319 A; 2694 C; 2538 G; 1347 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                     urological, hepatic, respiratory and vascular disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                           including neurological, endocrinological, cardiovascular,
                                                                         531 CTCTTCGGCCACTACTACTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTG 590
                                                                                                                                                                                        Local Similarity
CTGGTCTGCAACCCATGGTTCGAGCACGTGAGCATGCTGGTAATCATGCTCAACTGCGTG 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harpold M,
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                                                                                                                                                  Conservative
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                                                                                                                                              0; Mismatches 295;
                                                                                                                                                                                        Score 60; DB 20;
Pred. No. 9.2e-05;
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1004 GGCTGGCCTCCTGCGAACCGCTGCTTCCTGGACAGTGCCTTTGTCAGGAACAACAACCT 1063
                                                                         1011 CATTGTGGCTCTTCCTGGAAACAGCAGCCTGGCCCCTGCCCAATGGCTCGGCGCCCTGTGG 1070
                                                                                                                 944 CGTCCTTCTGCTCTTCGTCTTCATTTTCGGCATCGTTGGCGTCCAGCTCTG 1003
                                                                                                                                  951 GATCCTGGTGGTGGTCTACCTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGCGT 1010
                                                                                                                                                                           884 CGTGCCTAGCATGCGGATCCTGGTCACTCTGCTGGATACGCTGCCCCATGCTCGGGAA 943
                                                                                                                                                                                                       830 CCTCTCGGCTATCAGGACCG-----TGCGGGTGCTGCGCCCCTCCGCGCCATCAACCG 883
                                                                                                                                                                                                                                                    831 CCGCATGCTGAACATGCTCATCGTGTTTCCGCCTTCCTGCGTATCATCCCCCAGCATGAAGCC 890
                                                                                                                                                                                                                                                                                                                                                      711 GTCTTTGCCCTGGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGACGGGCTC 770
                                                                                                                                                                                                                                                                                             771 GATTTCTTCATCGTCGTGGCGGGC-ATGATGGAGTACTCGTTGGACGGACACAACGTGAG 829
                                                                                                                                                                                                                                                                                                                771 CTCACCGTTGTCCTGCTGGAGGCCCGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGAC 830
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Search completed: October 8, 2002, 08:09:01 Job time: 222 secs

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                    Score
               seq
seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383533 seqs, 122816752 residues
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                                                                                                                                                                                                                                                                                                                                                                 Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_NA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
     /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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   32207
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 US-08-984-709A-49
US-08-984-709A-51
US-08-940-40-354B-1
US-08-314-083B-1
US-08-316-257A-3
US-08-404-650-1
US-08-404-650-3
US-09-404-650-3
US-09-634-990-1
US-09-634-920-3
US-09-634-920-3
US-09-634-920-3
US-08-728-323A-1
US-09-426-998-3
US-09-426-998-3
US-09-426-998-3
US-09-426-998-3
US-09-426-988-3
US-09-426-988-3
US-08-770-379-20
US-08-757-669A-20
US-08-581-148C-3
US-08-232-305C-31
US-08-455-543A-31
US-08-455-543A-31
US-08-455-543A-3
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Sequence 1, Appli
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Sequence
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Sequence 51, Appl
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Sequence 22, Appl	Sequence 23, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 52, Appl	Sequence 208, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 43, Appl	Sequence 43, Appl	•	Sequence 43, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 6, Appli

ALIGNMENTS

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; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 249...7307
; OTHER INFORMATION:
US-08-984-709A-49
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US-08-984-709A-49
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                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 587-5360 INFORMATION FOR SEQ ID NO: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 420
CITY: La Jolla
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 7898 base pair
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 24.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
                                                                                                                           HYPOTHETICAL: I ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                       LENGTH: 7898 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ATTORNEY/AGENT INFORMATION:

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51, Application US/08984709A Patent No. 6320032
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                      SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1004
                                                                                                                                                                                  CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
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CITY: I
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                    APPLICATION NUMBER: FILING DATE: 02-DE
                                                                                              MEDIUM TYPE: Dis
COMPUTER: IBM CO
OPERATING SYSTEM:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                         4250 Executive Square,
                                                                             FastSEQ Version 1.5
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                    02-DEC-1997
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47.68;
                                                                                                                                                                                                                                                                                                                                                                HUMAN CALCIUM CHANNEL COMPOSITIONS AND
                                     US/08/984,709A
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Pred. No.
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                                                                                                                                                                                                   Sequence 1, Application Patent No. 5618720 GENERAL INFORMATION:
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                                                                    APPLICANT: Ellis, Steven Bradley
APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS
NUMBER OF SEQUENCES: 3
                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         1070 GGAGCTTCGAGCAGCTGGAGTACTGGGCCAACAACTTCGATGA 1112
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STREET:
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                                 ADDRESSEE:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 CATCCTGGAGGCCTTTGACGCCTTCATTTTCGCCTTTTTTGCGGTGGAGATGGTCATCAA
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             1660 Union Street
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Diego
                                   Brown, Martin,
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COMPUTER READABLE FORM:

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                                  RESULT 4
US-08-314-083B-1
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Sequence 1, Application US/08314083B Patent No. 5686241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                1760 CGCTGCTGCTGCTCTTCCTCTTCATCATCTTCG 1798
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                                                                                                                                                                                              1700 ACTGGACGTCGCTCAGCAACCTGGTGGCCTCCCTGCTCAACTCCATCCGCTCCATCGCCT 1759
                                                                                                                                                                                                                                                                          1640 CGCTGGGCATCTCCGTGTTGCGCTGCATCCGCCTCCTGAGGCTCTTCAAGATCACCAAGT 1699
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                                                                                                                                                     950 GGATCCTGGTGGTCTACTACGTATTTGCCATCATTG 988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/404,354B FILING DATE: 15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 6362-53192
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REGISTRATION NUMBER: 33,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 79...5700 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                   CCTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGA 829
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Pred. No. 0.0027;
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Best Local Similarity 49.0%;
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APPLICATION NUMBER:
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TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
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APPLICATION NUMBER: US 07/914,231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                  1640 CGCTGGGCATCTCCGTGTTGCGCTGCATCCGCCTCCTGAGGCTCTTCAAGATCACCAAGT 1699
                                                                                                                      1584 CGT----GGTGTGCAGCGGCATCCTGGAGCTGCTGGTGGAGTCGGGGGGCATGACGC 1639
                                                                                                                                                                                           1524 GATGTACGGGCTGGGCCTGCGCCAGTACTTCATGTCCATCTTCAACCGCTTCGACTGCTT 1583
                                                                                                                                                                                                                                                            1464 CTTGCAAGACATCGCCAATCGAGTGCTGCTGTCACTCTTCACCATCGAGATGCTGCTGAA 1523
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                                                                                                                                                                                                                                                                                               650 CATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAA 709
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830 CCCGCATGCTGAACATGCTCATCGTGTTCCGCTTCCTGCGTATCATCCCCAGCATGAAGC 889
                                                                                                                                                     770 CCTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGA 829
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OPERATING SYSTEM:
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"LECOMMUNICATION"
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 79...57
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                         Matches 166;
                                                                                                                                                       Query Match 3.5%;
Best Local Similarity 49.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
EPLING DATE: 08-NOV-1990
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                                                        1464 CTTGCAAGACATCGCCAATCGAGTGCTGCTGTCACTCTTCACCATCGAGATGCTGCTGAA 1523
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
710 GGTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTTGACGGGCT 769
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MEDIUM TYPE: Diskette
                                                                                           650 CATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAA 709
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
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                                                                                                                                                                                                                             NAME/KEY: Coding Sequence LOCATION: 79...5700 OTHER INFORMATION:
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
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CLASSIFICATION:
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                                                                                                                                                     Score 50.6; DB 1
Pred. No. 0.0027;
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                                                            Matches 166;
                                                                                                  Query Match
                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
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APPLICANT: Ellis, S
APPLICANT: Harpold,
APPLICANT: Campbell
TITLE OF INVENTION:
                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                 MOLECULE TYPE: Genomic DNA
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650 CATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                               LOCATION: 79...5700
OTHER INFORMATION: \product= "Alpha-1 subunit of animal calcium OTHER INFORMATION: channel"
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 54898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          950 GGATCCTGGTGGTGGTCTACTACGTATTTGCCATCATTG 988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/336,257A FILING DATE: 07-NOV-1994
                                                                                                                                                                                                          NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Ellis, Steven B.
Harpold, Michael M.
Campbell, Kevin P.
NVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
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                                                            Conservative
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                                                                          3.5%;
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                                                                          Score 50.6; DB Pred. No. 0.0027
                                                        Mismatches 169;
                                                                                          DB 1;
                                                                                            Length 5975;
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APPLICANT: Ellis, Steven Bradley
                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,599
FILING DATE: 27-JUNE-1007
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                                                                                                                                                  REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 630
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
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APPLICATION NUMBER: US 0:
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
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                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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FILING DATE: 13-JUL-1992
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                                                                                                                                                                                                                   NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,77
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                                 TYPE: nucleic acid
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                   STRANDEDNESS:
                                                         ENGTH:
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                                                       5975 base pairs
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Harpold, Michael Miller
                                                                                                                                       619-238-0062
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VENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
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linear
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              single
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US-09-404-650-1
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Matches 166;
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                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                Query Match
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APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILLING DATE: 199-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (19
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6816
TYPE: DNA
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                                                                                                                                       421
658 GGATTCTCAACTGCGTCTTCATTGTGCTACTACCTGTTGGAGTTGCTGCTCAAGGTCTTTG 717
                                                                                                                                                                         538 GCCACTACTACTTGACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTGTCCATTT 597
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                                                          481 GCATGTACCAGCCGTGCGACGACATGGACTGCCTGTCCGACCG---CTGCAAGATCCTGC 537
                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                217; Conservative
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Similarity 47.5%;
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Pred. No. 0.0064;
0; Mismatches 230;
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US-09-404-650-3
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Best Local Similarity 47.5%;
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dietrich, Paul S.
APPLICANT: MCGIVERN, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
TILE REFERENCE: R00418-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6855

TYPE: DNA

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (192)..(6755)
'711 CTGTCAGCCATCCGCACCGTGCGCGTCCTGAGGCCCTCAAAGCCATCAACCGCGTGCCC
                                                                                                                        778
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                                   838 CTGAACATGCTCATCGTGTTCCGCCTTCCTGCGTATCATCCCCAGCATGAAGCCGATGGCC 897
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                                                                             TCATCGTCATGGCAGG-----GATGGTCGAGTACTCCCTGGACCTTCAGAACATCAAC
                                                                                                                                                        CCCTGGGGATTTTTGGCAAGAAGTGCTACCTCGGGGACACATGGAACCGCCTGGATTTCT
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Pred. No. 0.0064;
0; Mismatches 230; Indels
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OF SECTIONOS: 4 UE: PatentIn Ver. 2.0 10 3 1: 6048	OFTWAR OFTWAR Q ID N	S
APPLICATI FILING DA PLICATION LING DATE PLICATION LING DATE	222222	
.1 -220-3 -3, Application US/09634920 - No. 6342357 - No. 6342357 - L INFORMATION: CANT: Splawski, Igor CANT: Keating, Mark T	ULT 11 09-634- equence atent N ENERAL APPLICA APPLICA TITLE O TITLE O	G P SES
GGAICCTGGIGGIGGICTACGIAGITIGCCATCATIG 988 	950 1808	Db
CGATGGCCGTGGTGGCCAGTACCGTCCTGGGCCTGGTGCAGAACATGCGTGCG	890 1748	рь Оу
CCCGCATGCTGAACATGCTCATCGTGTTCCGCTTCCTGCGTATCATCCCCAGCATGAAGC 889	830 1688	Qy Db
CCTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGA 829	770 1632	ФР
GGTCTTTGCCCTGGGCCTGCGAGGGTACCTGTCCTACCCCAGCAACGTGTTTGACGGGCT 769	710 1572	D Qy
CATCCTGGGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGGAGTTGCTGCTCAA 709	650 1512	Дb
tch 3.3%; Score 47.4; DB 6; Length 5962; al Similarity 48.4%; Pred. No. 0.017; lodels 4; Gaps 164; Conservative 0; Mismatches 171; Indels 4; Gaps	Query Mat Best Loca Matches	S HIV
T 10 25-5 25-6 25-7 25-8 25-9 APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL AMPBELL, KEVIN P. TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 9 CURRENT APPLICATION DATA: APPLICATION NATA: APPLICATION NUMBER: US/07/482,384 FILING DATE: 20-FEB-1990 ID NO:5: LENGTH: 5962	LT 025 025 ent AP CAM TI NU CU	RESU 5386 ; Pat ; M.; ; M.; ; SEQ ; SEQ
GTGGTGGTCTACTACGTATTTGCCATCATTGGGATCA 994	958 831	Db Db
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US-09-404-650-12
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LENGTH: 6503
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Matches 172; Conservative
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APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: AND USES
TITLE OF INVENTION: AND USES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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LOCATION: (1)..(6048)
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ORGANISM: Homo sapiens
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950 GGATCCTGGTGGTGGTCTACTACGTATTTGCCATCATTGGGATCAACTTGTTTAGAGGC 1008
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                                  CGCTGCGGCCCAGCTCGTGGTGCTCATGAAGACCATGGACAACGTGGCCACCTTCTGCA
                                                                                                                                                                                                        CCTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTGTGGGACATGA 829
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                                                                  ----TGCTGCGCACCTTCCGGTTGCTGCGGGTGCTGAAGCTGGTGCGCTTCATGCCGG
                                                                                                                                     CCCGCATGCTGAACATGCTCATCGTGTTCCCGCTTCCTGCGTATCATCCCCAGCATGAAGC 889
                                                                                                                                                                        CATCGTCATCAGCATCTGGGAAATCGTGGGGCAGGCGACGGTGGCCTGTCTG----
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47.9%;
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US-08-232-463-14
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                      Query Match
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APPLICANT: DORNER
                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: (703)836-9300
                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G
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                                                                                                                                        492 CCCGAGTACCAGTCTCCGTTTCTGCAGAGCGCCCAGTTCCTCTTCGGCCACTACTACTTT 551
                                                                                                                                                                                                 432 TGAAGTCCTATCCTCCATGGTGGGGGGAGGGAGCCTTCCCTCAGGCCACCCGCCGAGG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                GACTACCTGGGGAACCTCATCGCCCTGGCAAACCTGGTGTCCATTTGCGTGTTCCTGGTG 611
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                                                                                                                                                                                                                                              Query Match
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APPLICANT: Chang, Yuan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,278-0400
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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 2223 CTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTGCTCCTCCTGCTGCTGCTGCTC
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LOCATION:
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TOPOLOGY: li
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                                                                                                     TTGACGGGCTCCTCACCGTTGTCCTGCTGGAGGCCGGAGATGGTGGGCCTGCTGTCGCTG 819
                                                                   TGCTCCTGCTCCTGCTGCTCCTG-TTCATCCTGCTGCTGCTGCTCATCCTGCTGCTG
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1185 Avenue of the Americas
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Search completed: October
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SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 3
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 5
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APPLICANT: PYATI, JAYASHREE
APPLICANT: ZHU, JESSICA Y
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ORGANISM: HOMO SAPIENS
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Local Similarity 47.8%;
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Minimum DB seq length: 0
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Perfect score:
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1. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT: *
2. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT: *
3. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT: *
4. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT: *
5. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT: *
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIE

11	10	9	80	7	б	ъ	4	ω	2	1	Result No.
336	342	342	342	342	582.5	784	922	1020	1108	1671.5	Score
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AAM23901	AAG77820	AAB60097	AAG75376	AAB67465	AAM40803	AAU00502	AAB94563	AAW74828	AAM24447	AAM39017	ID
Rat EST encoded pr	Human ion channel	Human transport pr	Human colon cancer	_	Human polypeptide	Human TANGO 43/ Pr	Human protein sequ	Human secreted pro	Human EST encoded	Human polypeptide	Description

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175.5	175.5	175.5	178.5	178.5	180	180.5	182	184	184	186	186	186	186	186	186.5	186.5	187	187.5	187.5	189	189	189	189	189	189	190	190	190	190	190	195	208
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AAW37878	AAB10573	AAR/1000	AAW63139	AAR33547	AAY06300	AAY49431	AAY78900	AAB10593	AAR72607	AAY77544	AAW18390	AAW37711	AAR73055	AAB67469	AAB10581	AAR71009	AAP95645	AAY14594	AAY14595	AAB10582	AAR69604	AAR71010	AAY49430	AAY49429	AAR27648	AAB10568	AAW63149	AAW63137	AAR71002	AAR71001	AAR33545	AAM25607
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ALIGNMENTS

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CDT 21-JAN-2000; 25-APR-2000; 09-JUL-2000; 19-JUL-2000; 03-AUG-2000; 14-SEP-2000; 19-OCT-2000; Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; AAM39017 standard; Protein; 552 AA. Human polypeptide SEQ ID NO 2162. 22-OCT-2001 (first entry) 26-JUL-2001. WO200153312-A1. Homo sapiens leukaemia 26-DEC-2000; 29-NOV-2000; 2000US-0653450. 2000US-0662191. 2000US-0693036. 2000US-0488725. 2000US-0552317. 2000US-0598042. 2000US-0620312. 2000WO-US34263. 2000US-0727344

(HYSE-) HYSEQ INC.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
522 VELLERDILEEPEEDELTERLSOHPHLWLCR
                     455 VELLFRDILEEPGEDELTERLSQHPHLWLCR 485
                                                                                                                                                                                                                 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                       282 LEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEISTLAVYRLPHPGWRPEMVGLLSLW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 2162; 10078pp; English.
                                                                                                                                                                                                                                                                                                         232 WSCCSRSLPWACEGTCPTPATCLTG-------SSPLSCWRPEMVGLLSLW
                                                                                                                                                                                                                                                                                                                                                                                      194
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N-PSDB; AAI58173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                168 SLRFCRAPSSSSA-----TTTLTTWGT---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 QQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                 RGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLDA 394
                                                                YRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHKWDPRSHLQPLAGTPEATYQMT
                                                                                  YRRYSGPWSKIYFVLMWLVSSVIWVNLFLALILENFLHKWDPRSHLQPLAGTPEATVQMT 454
                                                                                                                                                                                                       DMTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLF
                                                                                                                                                                                                                                     DMTRMLNMLIVFRELRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLF
                                                                                                                                                                                                                                                                                                                                          LOSAQFLFGHYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNCVFIVYYL
                                                                                                                                                                                                                                                                                                                                                                          QTWCDFACSWCW------MQMCCLLSVMTSS------WGFSTASSLCTTC
                                                                                                                                                                                                                                                                                                                                                                                                          LLQVLQKVQLDSSHKQAMMEKVRSYGSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAFPQAVGVKPQN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLSSNVGEGGAFPQATRRGPST 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, LY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348;
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 1671.5; DB 2 68.1%; Pred. No. 9.3e-155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R, Ma Y,
, Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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AAM24447
                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 1256; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476164/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
                           456 ELLFRDILEEPGEDELTERLSQHPHLWLCR 485
                                                               121
                                                                                                                                             336 GVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLDAY 395
                                                                                                                                                                                             276 MTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYYVFAIIGINLFR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH99106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tomato; monkey; dog; sea urchin; expressed sequence tag; ES diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
181 ELLFRDILEEPGEDELTERLSQHPHLWLCR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2001; 2001WO-US02687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human EST encoded protein SEQ ID NO: 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM24447 standard; Protein;
                                                                                                                61 GVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFXAALVTLWNLMVVNNWQVFLDAY
                                                                                                                                                                             1 MTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFR 60
                                                      RRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHKWDPRSHLQPLAGTPEATYQMTV
                                                                       RRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHKWDPRSHLQPLAGTPEATYQMTV 455
                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                         210 AA;
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                                                                                                                                                                                                                                                           42.18; 99.58;
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Zhang J, Werhn
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man T;
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  970S-0040626

970S-0043311

970S-0043313

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97US-0038621.
97US-0040161.
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97US-0040333.
97US-00403336.
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         23 - MAY - 1997;
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25 - MAY - 1997;
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                                                                                                                                               New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                           Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS; Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA; Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
       This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 100 from the human cDNA clone HLQAB52 (deposited as clone ATCC 97901 and ATCC 209047).
                                                                                                                                                                                                                                            WPI; 1998-506364/43.
N-PSDB; AAV59610.
                                                                                                   Claim 1; Page 601-602; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN
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97US-0047611.
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97US-0047613.
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97US-0047633.
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97US-0056631.
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97US-0056884.
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97US-0056908.
97US-0056908.
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97US-0056910.
97US-0056911.
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97US-0057658.
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s-0056892.
s-0056893.
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Endress GA;

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ACC XXX ACC XX
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AAB94563
ID AAB9
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                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed is (see AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                                                                               11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:15339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94563 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSQHPHLWLCR 191
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                                                                                                                                                                                           Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                             99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                              Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.7%;
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Pred. No. 1.4e-91;
0; Mismatches 0;
                                                                                                                                                                                        Hayashi K, S
A, Nagai K,
                                                                                                                                                                                           Saito K,
K, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the Songlementary strand of a polynucleotide which comprises one of C the 5602 nucleotide sequences defined in the specification, where the CO oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the C complementary strand of a polynucleotide which comprises a 5'-end c sequence and an oligonucleotide comprising a sequence, where the C polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence of sequence, where the C oligonucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in the specification. The primers set useful for synthesising polynucleotides, c particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs challafor the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs casaily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH3742 represent human cDNA sequences; AAB92446 to AAB95893 represent buman amino acid sequences; AAB92446 to AAB95893 represent invention.
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  Human; TANGO 315; clone jthLaO45bO2; TANGO 330; cellular process regulator; gene therapy; mixed
                                                          Human TANGO 437 protein.
                                                                                                     18-JUL-2001
                                                                                                                                                                              AAU00502 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                  285
                                                                                                                                                                                                                                                                                                                      437
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                                                                                                                                                                                                                                                                                                                                                                                                                                          189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 AAFEVLSSMVGEGGAFPQATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTWCPFAC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 CWRPEMVGLLSLWDMTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 AAFEVLSSMYGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                         RSHLQPLAGTPEATYQMTVELLFRDILEEPGEDELTERLSQHPHLMLCR 485
                                                                                                                                                                                                                                                                                                                                                       -ILWNLMVVNNWQVFLDAYRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHKWDP
                                                                                                                                                                                                                                                                                                                                                                             VTLWNLMVVNNWQVFLDAYRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHKWDP 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYYVFAIIGINLFR-----GVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAAL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                  -HYYFDYLG-NLIALANLVSICVFLVLDADVLPAER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWCWMQMCCLLSVMTSSWGFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LLSAEEFQKLFNEL----DRSVVKEHPPRPEYQSPFLQSAQFL--FG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AMMEEVRSYGSV------
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                                                                                                 (first
                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%;
51.6%;
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Pred. No. 1.1e-81;
                                                                                                                                                                              AA
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TANGO 437;
lymphocyte
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  TANGO 480; reaction;
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Homo
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Domain
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28..30
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                 /note=
456..4
                                                                                                  /label 333..3
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                                                                                                                              species variation 288..312
467..486
                                438..443
                                                                                                                 313..435
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                                                                                                                                                                                                                                           205..207
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                                                                  392..395
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                                                                                                                                                                                                                                                                                                                                            123..128
       /label= Cytoplasmic_domain
                                        /label=
                                                                                                                         /label=
                                                                                                                                                 /note= "Alternatively this residue is Lys due
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                                                                                                                                                                                                                                                                                                                                                                                   ′label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                   'label= Ion_transport-like_domain
                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune-related disorder; pathogenic infection;
cell proliferative disorder; autoimmune disorder
                                                                                                                                                                                                                                                                                                    abel=
                                                ..455
                .466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Alternatively this residue is
                                                                                                                                                                                                                                                                                                                                                                                                                                    species variation"
                                                                                                                                                                                                                                                                                                                  "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             species variation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     species variation"
                       "N-myristylation site"
                                                                      "Protein kinase C phosphorylation
                                                                                                                                                                                                                 "Casein kinase II phosphorylation
                                                                                                                                                                                                                                "Protein kinase C phosphorylation
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                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation
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                                                                                       "N-myristylation site"
                                                                                                                                                                                 "N-myristylation site"
                                       Transmembrane_domain
                                                       Casein kinase II phosphorylation site
                                                                                                                                                                                                                                                                                                  Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                   "N-myristylation site"
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                                                                                                        Extracellular_domain
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                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Kirst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                disorders e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
       259
                                                                 211 WSLPEMASVGLLLAIHLCLFTMFGMLLFAGG-------KQDDGQDRERLTYFQNL
                                                                          18 WMVP----TGWVRGLELSLW------GGDPVVPWSCRFCSQQDDGQDRERLTYFQNL
                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                     2001-235372/24
                                       PESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYSQFRGY 124
LMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHRQA
                                PESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYSQFRGY
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                                                                                                 Conservative
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574..579
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561..5
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487..50
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                                                                                                        29.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 505
                                                                                                 21;
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gene therapy applications. Antisense nucleic acid molecules and expression vectors containing the TANGO nucleic acids are also described. Diagnostic assays can be used to detect genetic alterations in the TANGO nucleic acids and to identify compounds that bind to or modulate activity of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. TANGO 437 shows homology to human Gene 100. TANGO 437 nucleic acids and proteins may be used to diagnose, treat and monitor immune-related disorders, pathogenic infections, hepatic disorders (e.g. jaundice), cell proliferative disorders (e.g. lymphoma, cancer) and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence representing human TANGO 437 is isolated from cDN. clone jthia045b02 from a human mixed lymphocyte reaction cDNA library. TANGO 437 is 1 of 4 novel human transmembrane proteins which also includes TANGO 315 (AAU00498-AAU00499), TANGO 330 (AAU00500-AAU00501) and TANGO 480 (AAU00503). The nucleic acids encoding these proteins are useful as modulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases and inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Fig 19; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Transmembrane_domain
524..591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Transmembrane_domain 470..472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-myristylation site"
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Score 784; DB 2
Pred. No. 8e-68;
1; Mismatches
                                                                               DB 22;
                                                                                    Length 591;
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14-SEP-2000;
19-OCT-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                   immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI59959.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442253/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 5734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM40803 standard;
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  localised neuropathies and central
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                                                                                                                           invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPSMKPMAVVASTVLGLVQNMRAFGGILV 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
Wang Z,
                                                                                                                                                                                                        SEQ ID NO 5734; 10078pp; English.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressant;
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Xu C,
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lu C, Xue AJ,
Drmanac RT;
nervous system
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Best Local
                                                         28-JUL-1999;
18-AUG-1999;
14-MAR-2000;
                                                                                                                                                                                                                                                                        Calcium channel transport polypeptide; calcium trafficking; neural disorder; HIV-induced dementia; immune system disorder; rheumatoid arthritis; muscular disorder; muscle contractile dysfunction; reproductive disorder; gastrointestinal disorder; pulmonary disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                             cardiovascular disorder; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 AAB67465;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB67465 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assays for receptor activity, arthritis and inflammation, leukaemias \text{C.N.S} disorders.
                              (HUMA-) HUMAN
                                                                                                                       27-JUL-2000;
                                                                                                                                                    08-FEB-2001
                                                                                                                                                                                  WO200108635-A2
                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                             proliferative
                                                                                                                                                                                                                                                                                                                                                     Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 NLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYSQFR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFRFLRIIPSMKPMAVVASTVLGL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFRFLRIIPSMKPMAVVASTVLGL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPTPATCLTG-----SSPLSC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYLMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAFPQATRRGPSTSLRFCRAPSSSSA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSPESITSLIVLITTANNLFVLIPAYSKNRAYAIFFIVFTVIGSIFLMNLLTAIIYSQFR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSYPSNVFDGLLTVVLLVLEISTLVCTDCHTQAGGRRWWR-----LLSLWDMTRMLNMLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNLIALANLVSICVFLVLDADVLPAERDDFILGILNCVFIVYYLLEMLLKVFALGLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TTTLTTWGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYLMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----WQMCCLLSVMTSS------WGFSTASSLCTTCWSCCSRSLPWACEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAMMEKVRSYGSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFGHYYFDY
                                                                                                                                                                                                                                                                                                                                                     acid sequence of a calcium channel transport polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                            2000US-0189064
                                                                                                                       2000WO-US20392.
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                              GENOME SCI INC
                                                                                                                                                                                                                                             disorder; cancer;
                                                                          99US-0145958.
99US-0149446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 582.5; DB : Pred. No. 1.9e-48;
                                                                                                                                                                                                                                             lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                             carcinoma; breast cancer
                                                                                                                                                                                                                                                             renal disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WRPEMVGLLSLWDMTRMLNMLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SSPWQTWCPFACSWCW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a calcium channel transport polypeptide. The polynucleotides, polypeptides, and antibodies are useful for preventing, treating, or ameliorating diseases associated with anomalies in calcium trafficking across the plasma membrane. They are used to diagnose, detect and treat or prevent diseases or conditions such as neural disorders (e.g. HTV-Induced dementia), immune system disorders (e.g. rheumatoid arthritis), muscular disorders (e.g. muscle contractile dysfunction), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. arrhythmias), renal disorders, proliferative disorders, and/or cancerous diseases and conditions (e.g. lung carcinoma or breast cancer).
 colorectal carcinoma
                Human; colon cancer;
                                            Human colon cancer antigen protein SEQ ID NO:6140
                                                                                    03-SEP-2001
                                                                                                                    AAG75376;
                                                                                                                                                  AAG75376 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 256-257; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                     GVTSQTSHWSRLYFWTFYIVTMVV-MTIIVAFILEAFVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RERYLTFKALNQNNTPLLSLKDFYDIYEVAALKWKAKKNREHW-----FDELPRTALLI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMYGEGGAFPQATRRGPSTSLRFCRAPSSSS 179
                                                                                                                                                                                                                                                                       AYRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHK 433
                                                                                                                                                                                                                                                                                                                                                                          RPLQLLRLFKLKERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIVFPNCC
                                                                                                                                                                                                                                                                                                                                                                                                                                              TIYGVELFLKVAGLGPVEYLSSGWNLFDFSVTVFAFLGLLAL----ALNMEPFYFIVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKGINILVKSKAFQYFMYLVVAVNGVWILVETFMLKGGNFFSKHVPWSY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SVMTSSWGFSTASSLCTT---CW-----SCCSRSLPWACEGTCPTPATCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFNDIEKRKFKSLLLHKRTAIQHAYRLLISQRRPAG----ISYRQFEGLMRFYK-PRMSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YESTLENSIVSLEVLLTTANEPDYMMPSYSRNPWSCYFFIVYLSIELYFIMNLLLAVVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
                                                                                                                                                                                                                                                                                                       NTSTVADAYRWRNHTVGNRTV----VEEGYYYLNNFDNILNSFVTLFELTVVNNWYIIME
                                                                                                                                                                                                                                                                                                                                             NSSLAP - -
                                                                                                                                                                                                                                                                                                                                                                                                          R---FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-138604/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the plasma membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584 AA;
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                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GSSPL----SCWRP-----EMVGLLSLWDMTRMLNM-----LIVF
                                                                                                                                                                                                                                                                                                                                        ----ANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%;
            colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .48; Preq. NO. ....
e 71; Mismatches 158;
            cancer antigen; diagnosis; detection;
                                                                                                                                                    594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TWGTSSPWQTWCPFACSWCWMQMCCLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 342; DB 22;
Pred. No. 1.5e-24;
                                                                                                                                                    B
                                                                                                                                                                                                                                       461
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in calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 114; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer-associated nucleic acid molecules (N) the proteins are collectively known as colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 7588-7590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH34781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben
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03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2001.
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                                 287
                                                                  262
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                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                 60 YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                FKGINILVKSKAFQYFMYLVVAVNGVWILVETFMLKGGNFFSKHVPWSY-----LVFL
                                                                                                                                                                                                                                                                                               QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMYGEGGAFPQATRRGPSTSLRFCRAPSSSS 179
RPLQLLRLFKLKERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIVFPNCC
                             R---FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALPG
                                                              TIYGVELFLKVAGLGPVEYLSSGWNLFDFSVTVFAFLGLLAL-----ALNMEPFYFIVVL
                                                                                                                                                                ----SVMTSSWGFSTASSLCTT---CW-----SCCSRSLPWACEGTCPTPATCL
                                                                                                                                                                                                 RERYLTFKALNQNNTPLLSLKDFYDIYEVAALKWKAKKNREHW--
                                                                                                                                                                                                                                                                 TFNDIEKRKFKSLLLHKRTAIQHAYRLLISQRRPAG----ISYRQFEGLMRFYK-PRMSA
                                                                                                                                                                                                                                                                                                                                 YFSTLENSIVSLFYLLTTANFPDVMMPSYSRNPWSCVFFIVYLSIELYFIMNLLLAVVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                    117;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157137.
99US-0163280.
                                                                                                 GSSPL---SCWRP---
                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                    71;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 342;
Pred. No.
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                                                                                               EMVGLLSLWDMTRMLNM----LIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                    158;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 594;
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10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; immune disorder; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB60097 standard; Protein; 748 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide with a human transport protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200078953-A2
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                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 118-120; 165pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF27717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC
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                                                   254 TFNDIEKRKFKSLLLHKRTAIQHAYRLLISQRRPAG----ISYRQFEGLMRFYK-PRMSA 308
                                                                                                                                  194
                                                                                                                                                                                                             Local Similarity es 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHK 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSSLAP-----ANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLD
        ATTTLT.
                                                                                       QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMYGEGGAFPQATRRGPSTSLRFCRAPSSSS
                                                                                                                                YFSTLENSIVSLFVLLTTANFPDVMMPSYSRNPWSCVFFIVYLSIELYFINNLLLAVVFD
                                                                                                                                                                       YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang J,
                                                                                                                                                                                                                                                                                                                                 such as cancer.
                                                                                                                                                                                                                                                                                         748 AA;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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99US-0148177.
99US-0149357.
99US-0162287.
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Lu DAM, Au-Young J, I
                                                                                                                                                                                                           71;
                                                                                                                                                                                                             Score 342; DB 22;
Pred. No. 2.1e-24;
1; Mismatches 158;
          -TWGTSSPWQTWCPFACSWCWMQMCCLL-
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Patterson
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IC23927; human; ion channel 23927; gene therapy; screening assay; predictive medicine; pharmacogenetics; pain disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ion channel 23927 protein (IC23927).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RERYLTFKALNONNTPLLSLKDFYDIYEVAALKWKAKKNREHW-----FDELPRTALLI 362
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199..2
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178..195
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233..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and proteins may be used in screening assays, predictive medicine (e.g. diagnostic assays and pharmacogenetics) and treatment of disorders characterised by insufficient production of IC23927 (e.g. central nervous system disorders, pain disorders, or disorders of cellular growth, differentiation or migration). The IC23927 nucleic acids and proteins are also useful as targets for developing modulating agents to regulate a variety of cellular processes, such as: ion transport (e.g. ion conductance); membrane excitability and/or polarisation; synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transduction (e.g. pain signalinty and/or polarisation; synaptic transduction (e.g. pain signaling); cell activation; cell proliferation; cell growth; cell differentiation; cell migration and muscle contraction. Administration of a modulator of 123927 (especially by gene therapy) may be used to treat main or a main discorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the human ion channel 23927 (IC23927) protein, which is claimed in the invention. The ion channel family of proteins is a large family of membrane bound proteins responsible for a wide range of transport and signalling functions in cells. The invention comprises IC23927 proteins and nucleic acids. The IC23927 nucleic acids compared to the invention comprises IC23927 proteins and nucleic acids. The IC23927 nucleic acids acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used to treat pain or a pain disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated ion channel polypeptide IC23927 useful in screening assays and treatment of disorders, e.g., central nervous system disorders and pain
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                                                                                                                                                                              431 FKGINILVKSKAFQYFMYLVVAVNGVWILVETFMLKGGNFFSKHVPWSY------LVFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-FEB-2000; 2000US-0185938
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                                                                                                                                                                                                                                         377 RERYLTFKALNQNNTPLLSLKDFYDIYEVAALKWKAKKNREHW-----FDELPRTALLI 430
                                                                                                                                                                                                                                                                                                                                  120 QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAFPQATRRGPSTSLRFCRAPSSSS 179
                                                                                                                                                                                                                 213 ---- SVMTSSWGFSTASSLCTT---CW--
                                                                                                                                                                                                                                                                                                    322 TFNDIEKRKFKSLLLHKRTAIQHAYRLLISQRRPAG----ISYRQFEGLMRFYK-PRMSA
                                                                                                                                                                                                                                                                                                                                                                                  60 YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
                                    NSSLAP - -
                                                                                     R---FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALPG
                                                                                                                     TIYGVELFLKVAGLGPVEYLSSGWNLFDFSVTVFAFLGLLAL----ALNMEDFYFIVVL
 NTSTVADAYRWRNHTVGNRTV----VEEGYYYLNNFDNILNSFVTLFELTVVNNWYIIME
                                                            RPLQLLRLFKLKERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIVFPNCC
                                                                                                                                                                                                                                                                                                                                                                YFSTLENSIVSLFVLLTTANFPDVMMPSYSRNPWSCVFFIVYLSIELYFIMNLLLAVVFD 321
                                                                                                                                                -----GSSPL----SCWRP-----EMVGLLSLWDMTRMLNM-----LIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                816 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silos-santiago I;
                              ~ANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLD
                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%; Score 342; DB 22; 25.4%; Pred. No. 2.3e-24; Live 71; Mismatches 158;
                                                                                                                                                                                                                                                                       -----TWGTSSPWQTWCPFACSWCWMQMCCLL-
                                                                                                                                                                                                              --SCCSRSLPWACEGTCPTPATCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
 654
                                                                                                                                                   286
                                                                                                                                                                                483
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                                                                                                                                                                                Matches
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use \mbox{\ \ -\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 992-993; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; tomato; monkey; dog; sea urchin; expressed sequence tag; ES diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat EST encoded protein SEQ ID NO: 1426
145 RERYLTFKALNQNNTPLLSLKDFYDIYEVAALKWKATKNREHWVD-----ELPRTALLI 198
                                                                                                                                            120 QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMYGEGGAFPQATRRGPSTSLRFCRAPSSSS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001; 2001WO-US02687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001
                                                         180 ATTTLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AYRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHK 433
: ||::||: :::|: |: :: | || || :::
655 GVTSQTSHWSRLYFMTFYIVTMVV-MTIIVAFILEAFVFR 693
                                                                                                                                                                                                30 YESTLENSIVSLEVLLTTANEPDVMMPSYSRNPWSCVFFIVYLSIELYFIMNLLLAVVFD
                                                                                                                                                                                                                                               60 YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
                                                                                                TFNDIEKRKFKSLLLHKRTAIQHAYRLLISQRRPAG----ISYRQFEGLMRFYK-PRMSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-476164/51.
                                                                                                                                                                                                                                                                                                           115;
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Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH98560
                                                                                                                                                                                                                                                                                                                                                                                                      520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0491404.
; 2000US-0617746.
; 2000US-0631451.
; 2000US-0663870.
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou P,
                                                                                                                                                                                                                                                                                                                        12.8%; Score 336; DB 22; 25.0%; Pred. No. 4.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian XB,
JJ, Werhn
                                                                                                                                                                                                                                                                                                      72; Mismatches
                                                 ----TWGTSSPWQTWCPFACSWCWMQMCCLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Werhman
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man T;
                                                                                                                                                                                                                                                                                                   159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen R,
                                                                                                                                                                                                                                                                                                                                                  Length 520;
                                                                                                                                                                                                                                                                                                 Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     horse;
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                144
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RESULT 12
AAM25607
ID AAM25
XX AAM25
AC AAM25
XX 16-OC
XX Humal
XX Anti
XX Ant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antihacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiavascular; antianaemic; aneamia; antianaemic; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antialergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999;
21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM25607 standard; Protein; 395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ ID NO:1122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000; 2000WO-US35017.
AAH99166 to AAH99904 encode the human proteins given in AAM25963. The proteins can have activities based on the
                                                                                                            Claim 20; Page 232; 1217pp; English.
                                                                                                                                                                           Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                               N-PSDB; AAH99548
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-457603/49
                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease; Parkinson's disease; neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 GVTSQTSHWSRLYEMTEYIATMVV-MTIVAFILEAFVFR 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R---FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FKGINILVKAKAFQYFMYLVVAVNGVWILVETFMLKGGNFFSKHVPWSY-----LVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SVMTSSWGFSTASSLCTT---CW------SCCSRSLPWACEGTCPTPATCL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTSTVADAYRWRNHTVGNRTV----VEEGYYYLNNFDNILNSFVTLFELTVVNNWYIIME 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPLQLLRLFKLKERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIVFPNCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0488725.
2000US-0552317.
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           AAM25225 to
tissues and
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AAR33545
ID AAR3
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein.e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteopprosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disorders.
WPI; 1993-093936/11
                                                                                                                                                                                                                                                                                                                                                                          Sequence of the alpha 1D human calcium channel subunit.
                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR33545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR33545 standard; Protein; 2161 AA
                                   Williams ME;
                                                    Brenner R,
                                                                                                                                                                                                                 04-MAR-1993
                                                                                                                                                                                                                                                    W09304083-A
                                                                                     (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                           10-APR-1992;
                                                                                                                                            15-AUG-1991;
                                                                                                                                                                             14-AUG-1992;
                                                                                                                                                                                                                                                                                                                         Lambert Eaton
                                                                                                                                                                                                                                                                                                                                        Human calcium channel subunit; diagnosis; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 VGLLSLWDMTRMLNM-----LIVFR----FLRIIPSMKPMAVVASTVLGLVQNMRAFGGIL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 FVFR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 FLHK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 LIFYYSFAIVGMEFFCGIVFPNCCNTSTVADAYRWRNHTVGNRTV----VEEGYYYLNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 VVVYYVFAIIGINLFRGVIVALPGNSSLAP-----ANGSAPCGSFEQLEYWANNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 LGLLAL-----ALNMEPFYFIVVLRPLQLLRLFKLKERYRNVLDTMFELLPRMASLGLTL
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                                                      Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                         syndrome.
                                                                                                                           92US-0868354
                                                                                                                                            91US-0745206
                                                                                                                                                                                 92WO-US06903
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                                                      Feldman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 208; DB 22;
Pred. No. 1.2e-11;
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                                                      Harpold MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 395;
                                                        Mccue AF;
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RESULT 14
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          Human neuronal calcium channel subunit alpha 1D.
                                                      30-NOV-1995
                                                                                              AAR71001;
                                                                                                                             AAR71001 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The alpha 1D subunit cDNA was isolated using fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a probe to screen a cDNA library of a human neuroblastoma cell line, 1Mx32, to obtain clone alpha 1.36. This clone was used as a probe to screen additional IMx32 cell cDNA libraries to obtain overlapping clones which were then employed for screening until a sufficient series of clones to span the length of the nucleotide sequence encoding the human alpha 1D subunit were obtained, see AAQ37811. AAQ37812 provides the sequence of an alternative exon encoding the transmembrane domain of the alpha 1D subunit. The alpha 1D protein
                                                                                                                                                                                                                       727 IVCIYFIILFICGNYILLNVFLAIAVDN 754
                                                                                                                                                                                                                                                            405 ---IYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                            348 APANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK-- 404
                                                                                                                                                                                                                                                                                                                                                                     626 IFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF-----
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                                                                                                                                                                                                                                                                                                                                                                                                       291 IIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                             584 VSLFNRFDCFVVCGGITETILVELEIMSPLG------ISVFRCVRLLR 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      524 TEYWLVIVLVFLNTLTISSEHYNQPDWLTQIQDIANKVLLALFTCEMLVKMYSLGLQAYF 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   475 NTENVSGEGENRGCCGSL -- CQAISKSK -----LSRRWRRWNRFNRTRCRAAVKSV 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing Lambert Eaton syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding specific human calcium channel sub-units - used for identifying calcium channel agonists and antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ37811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 CR--SGWVAPNGGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rocar
                                                                                                                                                                                                                                                                                          -------NFDETQTKRSTFDNFPQALLTVFQILTGEDWNAVMYDGIMAYGGPSSSGM 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRMLNMLIVFRFLR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---WMQMCCL-LSVMTSS-----WGF---STASSLCTTCWSC-----CSRSLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QATRRGPSTSLRFCRAPSSSSATTLTTWGTSSPWQTWCPFACSWC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNTSMPTSETESV 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSLQTSLFRRRLGTRAAFEVLSSMVG------158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQCITMEGWTDVL---YWMNDAMGFELPWVYFVSLVIFGSFFVLNLVLGVLSGEFSKERE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVLLTTANNPDYMIPAYSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calculated Mr of 245,163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                    (first entry)
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18.7%;
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Pred. No. 2.2e-09;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The alpha 1D subunit cDNA has been isolated using fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a probe to screen a cDNA library of human neuroblastoma cell line IMR32, to obtain clone alpha1.36, This close was used as a probe to screen additional IMR32 cell cDNA libraries to obtain overlapping
291 IIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSL
                                 584 VSLFNRFDCFVVCGGITETILVELEIMSPLG------ISVFRCVRLLR 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calcium channel activity.
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                                                                                                      524 TFYWLVIVLVFLNTLTISSEHYNQPDWLTQIQDIANKVLLALFTCEMLVKMYSLGLQAYF 583
                                                                                                                                                                                                                                               415 KAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNTSMPTSETESV 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 116-126; 285pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1993;
05-NOV-1993;
                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                   127 KSLQTSLFRRRLGTRAAFEVLSSMVG-------EGG------AFP----- 158
                                                                                                                                                                                                                                                                                                                   358 FQCITMEGWTDVL---YWMNDAMGFELPWVYFVSLVIFGSFFVLNLVLGVLSGEFSKERE 414
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                                                                                                                                                                                                                                                                                                                                                                                               333 CR--SGWVGPNGGI-----
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                                                                                                                                                                                                                                                                                                                                                      72 LVLLTTANNPDVMIPAYSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLM 126
                                                                                                                                                                                                                                                                                                                                                                                                                          12 CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                        SWCWMQMCCL-LSVMTSS-----WGF---STASSLCTTCWSC-----CSRSLP--- 240
                                                                                                                                                                                                             -----QATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTWCPF------AC 201
                                                                                                                                                                          NTENVSGEGENRGCCGSL--CQAISKSK-----LSRRWRRWNRENRRCRAAVKSV 523
                                                                     ------WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRMLNMLIVFRFLR 290
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93US-0149097
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            TIPE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2161;
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                                                               The alpha 1D subunit cDNA has been isolated using fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a probe to screen a cDNA library of human neuroblastoma cell line in MR32, to obtain clone alpha1.36, This close was used as a probe to screen additional IMR32 cell cDNA libraries to obtain overlapping clones, which were then employed for screening until a sufficient series of clones to span the length of the nt seuence encoding the human alpha 1D subunit was obtd. Full-length clones were then constructed by ligating partial clones. AAQ84653 shows the nt sequence of the cDNA encoding the alpha 1D subunit. The Alpha 1D protein has a calculated Mr of 245,163. It contains four putative internal repeated sequence regions which represent 24 putative transmembrane segments. It mediates DHP-sensitive high-voltage, long-lasting calcium channel activity. AAQ84654 shows an alternative exon encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium channel subunit; antagonist; agonist; diagnosis; Lambert Eaton Syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human neuronal calcium channel subunit alpha 1D including alternative
                                                                                                                                                                                                                                                                                                                                  DNA encoding human calcium channel sub-unit(s) -developing prods. for studying calcium channels, obtaining agonists and antagonists
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05-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ84654
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                                                the IS6 transmembrane domain. The difference occurs in AAs 373
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                                                                                                                                                                                                                                                                                                                                                                                                                  1995-090900/12.
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93US-0149097
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IVCIYFIILFICGNYILLNVFLAIAVDN 754
                                                                                                                                                                                                 IIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                          -----QATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTWCPF-----AC 201
                                        ---IYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                  APANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK-- 404
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Result
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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WNLMVVNNW-QVFLDAY 395 :: : : : VFQLVTGEDWNSVMYNGI 624	LLSVMTSSWGFSTAS 225 : : LLSLFTIEMLLKMYGLGLRQ 490 LSGWRPEMYGLLSLMDMTRM 279	FIANL 112 :: :	NLD, MICHAEL IS AND METHODS Length 1872; Indels 178; Gaps 19;	Sequence 36, Appl Sequence 35, Appl Sequence 10, Appl Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Calcium Channel Compositions and TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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LENGTH: 2161 amino acids
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                                                                                                                                                                                                                                                                                                                                                    333 CR--SGWVGPNGGI-----
                                                524 TFYWLVIVLVFLNTLTISSEHYNQPDWLTQIQDIANKVLLALFTCEMLVKMYSLGLQAYF 583
                                                                                                                         475 NTENVSGEGENRGCCGSL--CQAISKSK-----LSRRWRRWNRFNRRRCRAAVKSV 523
                                                                                                                                                                                                   415 KAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNTSMPTSETESV 474
                                                                                                                                                                                                                                      127 KSLQTSLFRRRLGTRAAFEVLSSMVG------EGG------AFP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                      SWCWMQMCCL-LSVMTSS-----WGF---STASSLCTTCWSC-----CSRSLP---
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Ellis, Steven
Williams, Mark
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APPLICANT:
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PRIOR APPLICATION DATA:
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                                                                          FILING DATE: 04-APR-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                   FILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: May 3
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/745,206 FILING DATE: 15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/868, FILING DATE: April 10, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/223
FILING DATE: April 4, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 04-APR-1988
                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                   REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                        Seidman,
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Feldman, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
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                                                      Stephanie L.
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                                                                                                                 us 07/176,899
                                                                                                                                                                                                                               us 07/603,751
                                                                                                                                                                          WO PCT/US89/01408
                                                                                                                                                                                                                                                                                   US 07/482,384
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; Sequence 51, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 49:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 2161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
STREET: LUCC
CITY: San Diego
CTATE: California
                                                                                          APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUWAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 FQCITMEGWTDVL---YWMNDAMGFELPWVYFVSLVIFGSFFVLNLVLGVLSGEFSKERE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 LVLLTTANNPDVMIPAYSKNRAYA----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 71
                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSLFNRFDCFVVCGGITETILVELEIMSPLG-------ISVFRCVRLLR 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWCWMQMCCL-LSVMTSS------WGF---STASSLCTTCWSC-----CSRSLP--- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK-- 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTWCPF------AC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF-----
                                                          E: Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                     Harpold, Michael
Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
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internal
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SLP 240 3LQAYF 583	202 SWCMMOMCCL-LSVMYSSWGFSTASSLCTTCWSCCRSLP : : :	Qy 20 Db 52
	NTENVSGEGENRGCCGSL**CQALSNSN*****LSRKWRKWNRENKR	DD 4.
AC 201	QATERGPSTSLRFCRAPSSSSATTTLTTWG	
158 SETESV 474	127 KSLQTSLFRRRLGTRAAFEVLSSMVGEGGAFP	Qy 13 Db 41
FRGYLM 126 FSKERE 414	72 LVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLELMNLLTAIIYSQERGYLM 	Oy 7
ESLTSL 71 :: :: FAMLTV 357	12 CRLGGGWMYPTGWYRGLELSLWGGDPVYPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL : :: :: 333 CRSGWYGPNGGITNFDNFAFAMLTY	Qy 1 Db 33
176; Gaps	atch 7.2%; Score 190; DB 1; Length 216 cal Similarity 18.5%; Pred. No. 1.8e-09; 94; Conservative 83; Mismatches 155; Indels	Query Ma Best Loo Matches
	MOLECULE TYPE: procesn FRAGMENT TYPE: internal -08-455-543A-51	; FRA US-08-45
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	STICS	; INFO
	E: (619)	 E H E
	ON INFORMATI	
	NAME: Seidman, Stephanie L. PEGISTERATION NITMERE. 33 770	
	04-APR-1988	
	N H	PRI
	ING DATE: 04-APR-198	FIL
	PLICATION DATA:	; PRI
	APPLICATION NUMBER: US 07/482,384 EILING DATE: 20-FEB-1990	יייי קי
	FILING DATE: 30-NOV-1990	
	APPLICATION DATA:	PRIOR
	FILING DATE: April 10, 1992 TOB ADDITION DATA.	FIL:
	APPLICATION DATA:	PRIOR
	LICATION NUMBER:	
	FILING DATE: May 31, 1995 TOR ADDITON DATA:	PRIOR
	LICATION DATA:	; cur
	FastSEQ V	·. ·.
	MEDIUM TYPE: DISKETTE COMPUTER: IBM Compatible	o :
	READABLE FORM	COM.
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RESULT 5 US-08-223-305C-49

Sequence 49,

tent No.

GENERAL INFORMATION:

APPLICANT:
APPLICANT:

McCue, Ann

APPLICANT: APPLICANT:

Williams, Mark Feldman, Daniel Harpold, Michael Ellis, Steven

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES:

APPLICATION NUMBER: US 07 FILING DATE: 04-APR-1988 ATTORNEY/AGENT INFORMATION: NAME: Seidman, Stephanie

TELECOMMUNICATION INFORMATION:

NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516

APPLICATION NUMBER: WO POST FILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:

FILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: (

APPLICATION NUMBER:

FILING DATE:

20-FEB-1990

APPLICATION NUMBER: 1

APPLICATION NUMBER: US 0' FILING DATE: 15-AUG-1991

FILING DATE:

30-NOV-1990

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CURRENT AFFILIANTION NUMBER: US/08/223,300.

APPLICATION NUMBER: US/08/223,300.

FILING DATE: APFIL 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: APFIL 10, 1992

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/745,206
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TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 --- IYFVLWWLVSSVIWVNLFLALILEN 429
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5851824
                                                                                                US 07/176,899
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   (P519739)
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: INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino ...
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Harpold
APPLICANT: Ellis, (
APPLICANT: Williams
APPLICANT: Feldman
APPLICANT: MCCue, )
                                                                                                                                                                                                                                                                                      Sequence 51, Application US/08223305C Patent No. 5851824
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                                                                                          APPLICANT: Brenner, Robert TITLE OF INVENTION: HUMAN C TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 57
                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                    727 IVCIYFIILFICGNYILLNVFLAIAVDN 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                                                                                                        405 ---IYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 SWCWMQMCCL-LSVMTSS------WGF---STASSLCTTCWSC-----CSRSLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 KAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNTSMPTSETESV 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 FQCITMEGWTDVL---YWMNDAMGFELPWVYFVSLVIFGSFFVLNLVLGVLSGEFSKERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 CR--SGWVGPNGGI--
                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 18.5 nes 94; Conservative
   STATE:
                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 LVLLTTANNPDVMIPAYSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFYWLVIVLVFLNTLTISSEHYNOPDWLTQIQDIANKVLLALFTCEMLVKMYSLGLQAYF 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRMLNMLIVFRFLR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTENVSGEGENRGCCGSL--CQAISKSK-----LSRRWRRWNRFNRRRCRAAVKSV 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTWCPF-----AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSLQTSLFRRRLGTRAAFEVLSSMVG-----
                   San Diego
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California
                                   E: Brown, Martin,
1660 Union Street
                                                                                                                                                                                       Ellis, Steven
Williams, Mark
Feldman, Daniel
                                                                                                                                                                                                                                                Harpold, Michael
                                                                                                                                                                     McCue, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NFDETQTKRSTFDNFPQALLTVFQILTGEDWNAVMYDGIMAYGGPSSSGM 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%;
                                                                                              HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS
57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 190; DB 2,
Pred. No. 1.8e-09;
""Gmatches 156;
                                                         Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EGG-----AFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ISVFRCVRLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TNFDNFAFAMLTV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:

OPERATING SYSTEM: COMPUTER:

IBM Compatible

Diskette

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

92101-2926 California

COUNTRY:

USA

CITY: San Diego

STREET: ADDRESSEE:

1660 Union Street

Brown, Martin,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 18.5
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619)238-006 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/868,354
FILING DATE: APRII 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AGG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 04-APR-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/223,305C FILING DATE: April 4, 1994 PRIOR APPLICATION DATA:
241 ------WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRMLNMLIVERFLR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
                                                          524 TFYWLVIVLVFLNTLTISSEHYNQPDWLTQIQDIANKVLLALFTCEMLVKMYSLGLQAYF 583
                                                                                                    202 SWCWMQMCCL-LSVMTSS-----WGF---STASSLCTTCWSC-----CSRSLP--- 240
                                                                                                                                           475 NTENVSGEGENRGCCGSL--CQAISKSK-----LSRRWRRWNRFNRRRCRAAVKSV 523
                                                                                                                                                                                                                             415 KAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNTSMPTSETESV 474
                                                                                                                                                                                                                                                                                                            358 FQCITMEGWTDVL---YWVNDAIGWEWPWVYFVSLIILGSFFVLNLVLGVLSGEFSKERE 414
                                                                                                                                                                                                                                                                                                                                                                                                       333 CR--SGWVGPNGGI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     12 CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 71
                                                                                                                                                                                                                                                                                                                                                     72 LYLLTTANNEDVMIPAYSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                  -----QATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTWCPF-----AC 201
                                                                                                                                                                                                                                                                     KSLQTSLFRRRLGTRAAFEVLSSMVG------EGG------AFP----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2161 amino acids
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 190; DB 2; 18.5%; Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2161;
                                                                                                                                                                                                                                                                                                                                                                                                ---TNFDNFAFAMLTV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 176; Gaps
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414	358 FQCITMEGWTDVLYWMNDAMGFELPWYYFYSLVIFGSFFVLNLVLGVLSGEFSKERE	
126		
'1 157	QY 12 CRLGGGWWVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 7	
os 20;	Query Match 7.2%; Score 190; DB 2; Length 2161; Best Local Similarity 18.5%; Pred. No. 1.8e-09; Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps	
	MOLECULE TYPE: S-08-311-363-2	
	TELEFAX: (619)2 INFORMATION FOR SEQ	
	TELECOMMUNICATION INFORMATION: TELEPHONE: (619)238-0999	
	REGISTRATION NUMBER: 33,779 REFERENCE/DOCKET NUMBER: 6362-51506	
	ATTORNEY/AGENT INFORMATION:	
	FILING DATE: PRIOR APPLICATION DATA:	
	APPLICATION	
	COMPUTER: IBM PC COmpatible	
	STREET: 1660 Union Street	
	CORRESPONDENCE ADDRE ADDRESSEE: Brown,	
	NUMBER OF SEQUENCES: 32	
	TITLE OF INVENTION:	
	APPLICANT: MCCUe, AND APPLICANT: Brenner,	
	APPLICANT: Feldman,	
	APPLICANT: Harpold,	
	RESULT 7 US-08-311-363-2 J. Sequence 2, Application US/08311363 Fatent No. 5876958 Fatent No. 5876958	
	DD /4/ IVCIXETIHETCGNXILLINVELATAVDN /54	
	400 LIE VLWWLVSSVIWVNEFLALILEN	
/26	AGE	
404	348 APANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK	
676	020 LENVIKHWISHSNEVASHLINGMKSLASHLHHHELETILESHIGMQLEGGKE	
347	291 IIPSMKPMAVVASTVLGLVQNWRAFGGILVVVYYVFAIIGINLFRGVIVALPGNSSL	
625	384 VSLENKEDCEVVCGGITETILVELBIMSPLGISVFRCVRLLR	

US-08-336-257A-7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application Patent No. 5726035
GENERAL INFORMATION:
                                                                                                                                                                             TELEFAX: (619) 238-00
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jay, Scott D
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Campbell, Kevin P.
APPLICANT: Campbell, Kevin P.
APPLICANT: CALCIUM CHANNEL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                       MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1873 amino acids
                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 KAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNTSMPTSETESV 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 KSLQTSLFRRLGTRAAFEVLSSMVG-------EGG------AFP------ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        727 IVCIYFIILFICGNYILLNVFLAIAVDN 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 --- IYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 APANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK-- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   626 IFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFIIIIFSLLGMQLFGGKF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584 VSLFNRFDCFVVCGGITETILVELEIMSPLG-------ISVFRCVRLLR 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524 TEYMLVIVLVFLNTLTISSEHYNQPDWLTQIQDIANKVLLALFTCEMLVKMYSLGLQAYF 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 SWCWMQMCCL-LSVMTSS------WGF---STASSLCTTCWSC-----CSRSLP--- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 NTENVSGEGENRGCCGSL--CQAISKSK------LSRRWRRWNRFNRRRCRAAVKSV 523
                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                     NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 54898
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CONTROL OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 92101-2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Brown, Martin, Haller & McClain STREET: 1660 Union Street
                                                                     TOPOLOGY:
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08435675B Patent No. 5710250
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                            OPERATING SYSTEM: DOS
SOTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin,
                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 SRVFYWLVILIVALNTLSIASEHHNQPLWLTHLQDTANRVLLSLFTIEMLLKMYGLGLRQ 490
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                                      FILING DATE: 05
CLASSIFICATION:
                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                       CITY:
APPLICATION NUMBER:
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                                                   UMBER: US/08/435,675B
05-MAY-1995
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  US 08/314,083
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Pred. No. 1.8e-09;
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                                                                           Sequence 13, Application US/07745206A Patent No. 5429921
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                                                           GENERAL INFORMATION:
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                    APPLICANT:
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    APPLICANT:
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LENGTH: 1873 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 YEMSIENREDCEVVCSGILELLLVESGAMTP----LGISVLRC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 ---WCWMQMC-----SSWGFSTAS 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 VLGVLSGEFTKEREKAKSRGTFQKLREKQQLEEDLRGYMSWITQGEVMDVEDLREGKLSL 388
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STRANDEDNESS: sir
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
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APPLICATION NUMBER: US 0.
FILING DATE: 13-JUL-1992
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                                                                                                                                                                                                                                                                                                      RRYSGPWSK-----IYFVLWWLVSSVIWVNLFLALILENFLH-----KWDPRSHL 440
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Williams, Mark
                    Harpold, Michael
Ellis, Steven
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linear
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RESULT 11
US-08-311-363-13
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                                         Sequence 13, Application US/08311363 Patent No. 5876958
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GENERAL INFORMATION: APPLICANT: Harpol
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SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
                                                                                                                                                                    1373 YRMELSIFYVVYFVVFPFFFVNIFVALIIITFQEQGD 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1142 TSRWSFSWSSPAASPWLLRTQCAQTRPGTTLNTWITFSLVSLPLRWRSTWDCCFTLEP-- 1199
                                                                                                                                                                                                                                                      1313 DYEKEEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSPG 1372
                                                                                                                                                                                                                                                                                                                                      1253 LKAVFDCYVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGQYL 1312
                                                                                                                                                                                                                                                                                                                                                                                                                               1200 ISGTCGTFWTSLWSVAP--WWR-----LLSRSKGKDINTIKSLRVLRVLRPLKTIKRLPK 1252
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             358 SFEQLEYWAN-----NFDDFAAALVTLWNLMVVNNWQVFL----DAYRRYSGPWS- 403
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TITLE OF INVENTION: Human Calcium Channel Compositions
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 TSSPWQTW-CPFACSWCWMQMCCLLSVMT--SSWGFSTASSL---CTTCWSCCSRSLPWA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 SMVGEGGAFPQAT------RR------GPSTSLRFCR-APSSSSATTTLTTWG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 CEGTCPTPATCLTGSSPLSCWRPEMVGLLSL----WDMTRMLNMLIVFRFLRIIPSMKP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 7.0%; Score 185.5; DB 1; Local Similarity 24.6%; Pred. No. 3.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                    MAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALPGNSSLAPANGSAPCG 357
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135 S. LaSalle
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Harpold, Michael Ellis, Steven Williams, Mark Feldman, Daniel

McCue, Ann Brenner, Robert

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; Patent No. 5792846
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GENERAL INFORMATION:
APPLICANT: Harpold
APPLICANT: Ellis,
APPLICANT: William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619)238-0062 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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LENGTH: 1754 amino acids
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REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (619)238-0999
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1200 ISGTCGTFWTSLWSVAP--WWR-----LLSRSKGKDINTIKSLRVLRVLRPLKTIKRLPK 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1142 TSRWSFSWSSPAASPWLLRTQCAQTRPGTTLNTWITFSLVSLPLRWRSTWDCCFTLEP-- 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1082 ALLGKPRSFPVVTWTWKAKORGRRRWKRMTGAAPGLSSHTAPCSVAPPTCSAASATTSPG 1141
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                                                                                                                                                                                                                      1373 YRMELSIFYVVYFVVFPFFFVNIFVALIIITFQEQGD 1409
                                                                                                                                                                                                                                                                                                           1313 DYEKEEVEAQPROWKKYDFHYDNVLWALLTLETVSTGEGWPMVLKHSVDATYEEOGPSPG 1372
                                                                                                                                                                                                                                                                                                                                                                                                1253 LKAVFDCYVNSLKNVLNILIVYMLFMFIFAVIAVOLFKGKFFYCTDESKELERDCRGQYL 1312
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                                                                                                                                                                                                                                                                404 -----KIYFVLWWLVSSVIWVNLFLALILENFLHKWD 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSSPWQTW-CPFACSWCWMQMCCLLSVMT--SSWGFSTASSL---CTTCWSCCSRSLPWA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83; Conservative
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    Ellis, Steven Williams, Mark
                                             Harpold, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 185.5; DB 2; 24.6%; Pred. No. 3.7e-09; ative 54; Mismatches 141;
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INFORMATION FOR SEQ
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APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
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ADDRESSEE: Brown, Martin, Haller & McClain
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APPLICATION NUMBER: 08/223
FILING DATE: April 4, 1994
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
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PRIOR APPLICATION DATA:
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                                  101 FTVIGSLELMNLLTAIIYSQE-----
                                                                       332 CKPGWDG-PKHGITNFDNFAFAMLTVFQCITMEGWTDVL---YWVNDAVGRDWPWIYFVT 387
388 LIIIGSFFVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08 FILING DATE: May 31, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                          46 CSQQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYA----IFFIV 100
                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/603,751 FILING DATE: 04-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/482,384
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                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                Conservative
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18.4%;
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HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
: 57
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                                                                                                                                              score 178.5; DB 1; pred. No. 2.1e-08; 80; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6362-52517
                                        -----RGYLMKSLQTSLF 134
                                                                                                                                                                                     Length 1968;
                                                                                                                                                    Indels 205; Gaps
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on US/08223305C Michael Steven S, Mark , Daniel Ann Robert HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS 57 SSS: 57	ESULT 13 S-08-223-305C-45 Sequence 45, Application US/08223305C PATEENT NO. 5851824 GENERAL INFORMATION: APPLICANT: HILLIS, Steven APPLICANT: Williams, Mark APPLICANT: Feldman, Daniel APPLICANT: MILLIAMS, METHODS NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS: 57 COUNTRY: USA ZIP: 92101-2926 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ VETSION 1.5 APPLICATION NUMBER: 07/868,354 FILING DATE: APPLICATION DATA: APPLICATION NUMBER: US 07/745,206 FILING DATE: 15-AUG-1991 PRIOR APPLICATION NUMBER: US 07/745,206 FILING DATE: 30-NOV-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/745,206 FILING DATE: 30-NOV-1990 PRIOR APPLICATION DATA:
EKPAVGESKE 826	PAVGESKE
EEPGEDELTE 473	ILEEPGEDELTE 47
: :)b 752 MLVCIYFIILFISGNYILLNVFLAIAVDNL
LHKWDPRSHLOPLAGTPEA 4	29 405IYFVLWWLVSSVIWVNLFLALILENF-
LAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNW-QVFLDAYRRYSGPWSK- 400	2Y 347 LAPANGSAPCGSFEQLEYWANNFDDFAAAL : :::: : : : 55 703NFDEMQTRRSTEDNFPQSL
7	663
YVFALIGINLFRGVIVALPGNSS 3	290 RIIPSMKPMAVVASTV
EGTCPTPATCLIGSSPLSCWRPEMVGLLSLWDWTRMLNWLIVFRE	29 230 TCWSCCSRSLPWACEGTCPTPATCLTGSSF
FLVFUNTLTIASEHYNQPNWLTEVQDTANKALLALFTAEMLLKMYSLGLQAYEVSLFNRF 61	Db 557 FLVFLNTLTIASEHYNQPNWLTEVQDTANK
HRISKSKFSRYWRRWNRFCRRKCRAAVKSNVFYWLVI 55	506 GGDIEGENCGARLAHRISKSK
	QY 163RGPSTSLRFCRAPSSSSATTTLTTWC
-MLDQKKGKFAWFSHSTETHVSMPTSETESVNTENVA	Db 448 XPENEDEGMDEEKPRNRGTPAGMLDQKK
-RRLGTRAAFEVLSSMVGEGGAFPQATR	Qy 135 RRRLGTRAAFEVLSSM

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; FRAGMENT TYPE: internal
US-08-223-305C-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.8%; Score 178.5; DB 2; Length 1968; Best Local Similarity 18.4%; Pred. No. 2.1e-08; Matches 104; Conservative 80; Mismatches 175; Indels 205;
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APPLICATION NUMBER: US 07/176

FILING DATE: 04-APR-1988

ATTORNEY_AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 5251

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEPAX: (619)238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 45:
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LENGTH: 1968 amino acids
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FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
812 K------QELVEKPAVGESKE 826
                                                                                                                               405 ----IYFVLWWLVSSVIWVNLFLALILENF------LHKWDPRSHLQPLAGT--PEA 449
                                            450 TYQMTVELLFRDILEEPGEDELTE 473
                                                                                    752 MLVCIYFIILFISGNYILLNVFLAIAVDNLADAESLTSALKEEEEEKERKKLARTASPEK 811
                                                                                                                                                                            703 -----NFDEMQTRRSTFDNFPQSLLTVFQILTGEDWNSVMYDGIMAYGGPSFPG 751
                                                                                                                                                                                                               347 LAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNW-QVFLDAYRRYSGPWSK- 404
                                                                                                                                                                                                                                                                                                                     290 RIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSS 346
                                                                                                                                                                                                                                                                                                                                                                    617 DCFVVCGGILETI---LVETKIMSPLGISVLRC----VRLLRIFKITRYWNSL----- 662
                                                                                                                                                                                                                                                                                                                                                                                                                 230 TCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRMLNMLIVFRFL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 FLVFLNTLTIASEHYNQPNWLTEVQDTANKALLALFTAEMLLKMYSLGLQAYFVSLFNRF 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             506 GGDIEGENCGARLAHRISKSK------FSRYWRRWNRFCRRKCRAAVKSNVFYWLVI 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 -CCLLSVMT-----SSW------GFSTASSLCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 ----RGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTWCPFACSWC------WMQM 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 XPENEDEGMDEEKPRNRGTPAG--MLDQKKGKFAWFSHSTETHVSMPTSETESVNTENVA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 R-----RRLGTRAAFEVLSSMVGEGGAFPQATR------ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 LIIIGSFFVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 FTVIGSLFLMNLLTAIIYSQF------134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 CKPGWDG-PKHGIINFDNFAFAMLTVFQCIIMEGWTDVL---YWVNDAVGRDWPWIYFVI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/US89/01408 FILING DATE: 04-APR-1989
                                                                                                                                                                                                                                                                             ------SNLVASLLNSVRSIASLLLLLFLFIIIFSLLGMQLFGGKF------ 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-455-543A-48
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GENERAL INFORMATION:
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Best Local Similarity 19.6 Matches 105; Conservative
                                           Query Match
                                                                                                                                                                                                                                     TELEFAX: (619)238-006
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
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APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: May 31, PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
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                                                                                                   MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-APR-PRIOR APPLICATION DATA:
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SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/868, FILING DATE: April 10, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
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                                                                                                                                                                                                                                                                                                          NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 30-NOV
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                                                                                                                                         TOPOLOGY:
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                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                             2237 amino acids
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Ellis, Steven
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Feldman, Daniel
                                                                                                                                                                                                                                                        (619)238-0062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown, Martin, Haller & McClair
                                                                                                                                         linear
                                                                                                                                                                                                                                                                        (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER: WO PCT/US89/01408
04-APR-1989
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                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1988
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                                                                                                                     protein
                                                                                                                                                           single
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     6.7%; Score 175.5; DB 1; 19.6%; Pred. No. 5.1e-08; tive 89; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                            us 07/176,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/455,543A
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                                                                                                                                                                                                                                       48:
                                             Length 2237;
           Indels 157;
           Gaps
               24;
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US-08-223-305C-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                 APPLICATION NUMBER: 07/868,354
FILING DATE: APPLI 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brenner, Robert TITLE OF INVENTION: HUMAN (TITLE OF INVENTION: METHODS
                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492 VALNTLCVAMVHYNQPRRLTTTLYFA----EFVFLGLFLTEMSLKMYGLGPRSYFRSSF 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 EEGEDRFADLCAVGSPFARASLKSGKTESSSYFRRKEKMFRFFIRRMVKAQSFYWVVLCV 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 RRQQQIERELNGYLEWIFKAEEVMLAEEDR--NAEEKSPLDVLK--RAATKKSRNDLIHA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 SLOTSLERRRLG-TRAAFEVLSSMVGEGGAFPQATRRGPSTSLRFCRAPSSSSATTTLTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 IL---YNTNDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 EPVGDFPCGKEAPARLC--EGDTECREYWPGPNFGTTNFDNILFAILTVFQCITMEGWTD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 DTFPAAILTVFQILTGEDWNAVM--YHGIESQGGVSKGMFSSFYFIVLTLFGNYTLLNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 RAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705 LAIAVDN-------------LANAQELT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 DPVVPWSC-----RFCSQQDDGQDRE-----RLTYFQNLPESLTSLLVLLTTANNPD 82
                                                                                                                             APPLICATION NUMBER: US/08/223,305C FILING DATE: April 4, 1994
                                                                                                                                                                                                   COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
             FILING DATE:
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCFDFGVIVGSVFEVVWAAIKPGSSFGISVLRALRLLRIFKVTKYWSSLRNLVVSLLNSM 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSIISLLFLLFLFIVVFALLGMQLFGGQF---
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                                                                                                                                                                                                                                                                                  92101-2926
                                                                                                                                                                                                                                                                                                                                                              1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams, Mark
Feldman, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harpold, Michael
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                 15-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899
FILING DATE: 04 APR-1988
ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
FRAGMENT TYPE:
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APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
                                    423 LALILENFLHKWDPRSHLQPLAGTPEATYQMTVELLFRDILEEPGEDELTERLSQ 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
         705 LAIAVDN---
                                                                                647 DTFPAAILTVFQILTGEDWNAVM--YHGIESQGGVSKGMFSSFYFIVLTLFGNYTLLNVF
                                                                                                                         370 DDFAAALVTLWNLMVVNNWQVFLDAYRRY-----SGPWSKIYFVLWWLVSSVIWVNLF 422
                                                                                                                                                                         607 KSIISLLFLLFLFIVVFALLGMQLFGGQF----
                                                                                                                                                                                                              313 RAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNF 369
                                                                                                                                                                                                                                                       547 NCFDEGVIVGSVEEVVWAAIKPGSSEGISVLRALRLLRIEKVTKYWSSLRNLVVSLLNSM 606
                                                                                                                                                                                                                                                                                                 267 -----MVGLL--SLWDMTRM-----LNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNM 312
                                                                                                                                                                                                                                                                                                                                          492 VALNTLCVAMVHYNQPRRLTTTLYFA-----EFVFLGLFLTEMSLKMYGLGPRSYFRSSF 546
                                                                                                                                                                                                                                                                                                                                                                                   210 -CLLSVMTSSWGFSTASSLCTTCWSCCSRSLPWACEGTCPTPATC-LTGSSPLSCWRPE- 266
                                                                                                                                                                                                                                                                                                                                                                                                                                 432 EEGEDRFADLCAVGSPFARASLKSGKTESSSYFRRKEKMFRFFIRRMVKAQSFYWVVLCV 491
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 RRQQQIERELNGYLEWIFKAEEVMLAEEDR--NAEEKSPLDVLK--RAATKKSRNDLIHA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 SLQTSLFRRRLG-TRAAFEVLSSMVGEGGAFPQATRRGPSTSLRFCRAPSSSSATTTLTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 IL---YNTNDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKL 375
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linear
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Search completed: October 8, 2002, 10:06:49 Job time : 31 secs

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Database
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length: 2000000000
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2: pir2:*
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Gapop 10.0 , Gapext 0.5
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 Maximum Match 100%
Listing first 45 summaries
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A45290
S11339
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protein C48A7.1 [i calcium channel al	sodium channei pro sodium channel pro probable voltage-g	D	channel channel channel	calcium channel BI calcium channel al calcium channel pr sodium channel hom

ALIGNMENTS

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two-pore calcium channel protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Ate: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: JC7240
R;Ishibashi, K; Suzuki, M.; Imai, M.
Blochem. Blophys. Res. Commun. 270, 370-376, 2000
A;Title: Molecular cloning of a novel form (two-repeat) protein related to voltage-ga
A;Reference number: JC7240
A;Accession: JC7240
A;Accession: JC7240
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JC7240
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A; Note: DKFZp434M0223.1
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R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp434M0223.1 - C; Species: Homo sapiens (man) C; Date: 04-Feb-2000 #sequence_revision
A; Molecule type: mRNA
A; Residues: 1-819 <ISH>
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A;Molecule type: mRNA
A;Residues: 1-371 <AAA>
A;Cross-references: EMBL:AL137479
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A; Accession: T46421
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Similarity 99.6%;
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Pred. No. 1.4e-87;
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Qy 115 AIIYSQFRGYLMKSIQ-TSLFRRRLGTRAAFEVLSS 149 :: : : :	QY 55 RERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIEFIVETVIGSLELMNLLT 114 :: : : : :	Query Match 13.0%; Score 342; DB 2; Length 724; Best Local Similarity 24.1%; Pred. No. 1.1e-19; Matches 115; Conservative 84; Mismatches 144; Indels 134; Gaps 19;	C;Genetics: A;Gene: AT4g03560 A;Map position: 4	A; Molecule type: DNA A; Residues: 1-724 <sto> A; Cross-references: GB:NC_001268; NID:g7270679; PIDN:CAB77841.1; GSPDB:GN00140</sto>	A; Pitle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Reference number: A85001; MUID:20083488 A; Recession: B85045 A; Accession: B85045	Sequencing Co	le calc les: Ar	Qy 398 YSGPWSKIYFYLWWLVSSVIWVNLFLALILENFLHK 433	QY 343 GNSSLAPANGS-APCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLDAYRR 397	QY 288FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALP 342	QY 256GSSPLSCWRPEMVGLLSLWDMTRMLNMLIVFR- 287	211 LLSVMTSSWGFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLT- :::::		Qy 120 QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAF	YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVETVIGSLFLMNLLTAIIYS	Query Match 13.1%; Score 345; DB 2; Length 819; Best Local Similarity 25.7%; Pred. No. 7e-20; Matches 117; Conservative 71; Mismatches 164; Indels 104; Gaps 18;	A;Cross-references: DDBJ:AB018253 A;Experimental source: kidney C;Comment: This protein is a phosphorylated transmembrane glycoprotein having characteri C;Keywords: glycoprotein; kidney; transmembrane protein
Db 583 LALFTCEMLVKMYSLGLQAYFVSLFNRFDCFVVCGGITETILVELEIMSPLGISVFRCVR 642	230 TCWSCCSRSLEWACEGTCPTPATCLTGSSP	1/3 KAPSSSATTTETTWEITSSPWLIWCFFALSWCMWNDMCCLLSVRISSWGFSKASSLCT	410SKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNT	Db 358 FQCITMEGWTDVLYMVNDAIGWEWPWYYFVSLIILGSFFVLNLVLGVLSGEF 409 Qy 127 KSLQTSLFRRRLGTRAAFEVLSSWGEGGAFPQATRRGPSTSLRFC 172	Db 333 CR-SGWVGPNGGI	CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTVFQNLPESLTSL 71	Query Match 7.5%; Score 197; DB 2; Length 2181; Best Local Similarity 18.2%; Pred. No. 1.7e-07; Matches 93; Conservative 81; Mismatches 175; Indels 162; Gaps 17;	A; Molecule type: mRNA A; Residues: 1-2181 <sei> A; Residues: 1-2181 <sei> A; Cross-references: GB:M83566; NID:g179751; PIDN:AAA35629.1; PID:g179752 A; Experimental source: pancreatic beta cells C; Superfamily: voltage-dependent calcium channel protein alpha-1 chain C; Keywords: membrane protein; voltage-gated ion channel</sei></sei>	A; Selno, S.; Chen, L.; Selno, M.; Blonder, C.; Taxeda, J.; Johnson, J.H.; Bell, G.I. Proc. Natl. Acad. Sci. U.S.A. 89, 584-588, 1992 A; Title: Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expres A; Reference number: A38198; MUID:92115705 A; Accession: A38198	s: Homo sapiens (man) 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000 ion: A38198	RESULT 4 A38198 A38190 Calcium channel alpha-1 chain, pancreatic - human N.Alternate names: beta-cell-type calcium channel alpha-1 chain; neuroendocrine-type	QY 380 WNLMVVNNWQVELDAYRRYSGPWSKI-YEVLWWLVSSVIWVNLFLALILENELHKWD 435	QY 324 YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTL 379 :: :: : : :	QY 264 RPEMVGLISLWDMTRMLNMLIVEREFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY 323	210 CLLSVMTSSWGESTASSICTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCW :	QY 168 SLR-FCRAPSSSATTTLTTWGTSSPWQTWCPFACSWCW-MQMC 209	150NVGEGGAFPQATRRGPST

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671	615 FNLLVMGNWQVWMESYKDLTGTWWSITYFVSFYVITILLLLNLVVAFYLEAFFTELD 671	615	₽
435	WNLMYVNNWQVFLDAYRRYSGEWSKI-YFVLWWLVSSVIWVNLFLALILENFLHKWD 435	380	Ϋ́
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VVY 323		264	δ
508	472LKIYIYGFENYWREGANREDELVIWVIVIGETATEIT	472	В
SCW 263	CLLSVMTSSWGFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCW	210	Ωy
EMA 471	413 QLRAFVRSPNEGYAISFILIINFIAVVVETTLDIEESSAQKPWQV-AEFVEGWIYVLEMA 471	413	₽
ОМС 209	S	168	Ωy
LSQ 412	353 KISKEEFGLIFDELDDTRDFKINKDEFADLCQAIALRFQKEEVPSLFEHFPQIYHSALSQ	353	Ъ
PST 167	150MVGEGGAFPQATRRGPST 167	150	Ωy

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residue

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conceptual

L.H.; chann

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voltage-dependent calcium channel alpha 1E - rat C; Species: Rattus norvegicus (Norway rat) C; Date: 24-Feb-1994 #sequence_revision 18 Nov-1994 #text_change 24-Sep-1999 C; Accession: A37490 R; Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, Science 260, 1133-1136, 1993 Science 260, 1133-1136, 1993 A; Title: Structure and functional expression of a member of the low voltage A; Reference number: A37490; MUID:93262464 A; Accession: A37490
A; Status: preliminary; not compared with conceptual translation a.Malon.ia trans.
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A; Note: sequence extracted from NCBI backbone (NCBIP:132101)
C; Superfamily: voltage-dependent calcium channel protein alp
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A; Residues: 1-2222 <SOO>
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Best Local :
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           477
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                                              663 LTKDEQEEEEAFNQKHALQKAKEVSPMSAPNMPSIERDRRRRHHMSMWEPRSSHLRERRR
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                                                                                                                                                                             NLMVVNNW-QVFLDAYRRY----SGPWSKIYFVLWWLVSSVIWVNLFLALILENFL----
                                                                                                                                                                                                                                                                                                                                                       L--SLWDMTRM-----LNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY 323
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                                                                                                                                    QILTGEDWNEVMYNGIRSQGGVSSGMWSAIYFIVLTLFGNYTLLNVFLAIAVDNLANAQE
                                                                                                                                                                                                                         ---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLW
                                                                                                                                                                                                                                                                                                               IFEVVWAIFRPGTSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLF
                                                                                                                                                                                                                                                                                                                                                                                                     VHHNQPQWLTHLLYYAEFLFLGLFLLEMSLKMYGMGPR----LYFHSSFNCFDFGVTVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTWGT----SSPWQTWCPFACSWCWMQMCCLLSV--MTSS----WGFSTASSLCTTCWSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLRIFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF-----
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voltage-dependent Ca2+ channel alpha 1-subunit - golden hamster C;Speckes: Mesocricetus auratus (golden hamster) C;Date: 27-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000 C;Accession: A46227
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A;Cross-references: GB:L29346; NID:g522330; PIDN:AAA59206.1; PID:g522331
A;Note: authors translated the codon AGG for residue 788 as Lys, and CCTC;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L. J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium A;Reference number: A54972; MUID:94350992
A;Accession: C54972
A;Status: preliminary; nucleic acid sequence not shown; not compared with concep A;Molecule type: mRNA
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C;Species: Mus musculus (house mouse)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C;Accession: C54972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 TTWGT----SSPWQTWCPFACSWCWMQMCCLLSV--MTSS----WGFSTASSLCTTCWSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 LWGGDPVVPWSCRFCSQQDDGQD----RERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                                                                                                                RH
                                                                                                                                                                                                                                                                                                                                                    QILTGEDWNEVMYNGIRSQGGVSSGMWSAIYFIVLTLFGNYTLLNVFLAIAVDNLANAQE
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Pred. No. 3.1e-07;
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R;Yaney, G.C.; Wheeler, M.B.; Wei, X.; Perez-Reyes, E.; Birnbaumer, L.; Boyd III, A.E.; Mol. Endocrinol. 6, 2143-2152, 1992
A;Title: Cloning of a novel alpha 1-subunit of the voltage-dependent calcium channel from A;Reference number: A46227; MUID:93149124
A;Accession: A46227
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A; Note: sequence extracted from NCBI backbone (NCBIP:123692)
C; Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                   A; Experimental source: neuroblastoma, cell line IMR32 C; Comment: This protein is a subunit of the voltage-dependent calcium channel. C; Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                         C; Species: Homo sapiens (man)
C; Date: 30-Jun-1992 #sequence_revision
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F;164-183/Domain:
                       C; Keywords: transmembrane protein F;127-145/Domain: transmembrane #:
                                                                                                                                                A; Residues: 1-2161 <WIL>
A; Cross-references: GB:M76558
                                                                                                                                                                                                                      A; Reference number: JH0564; A; Accession: JH0564
                                                                                                                                                                                                                                                  A; Title: Structure and functional expression of alpha1, alpha2, and beta subunits A; Reference number: JH0564; MUID: 92110010
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                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                 R;Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B.; Neuron 8, 71-84, 1992
                                                                                                                                                                                                                                                                                                                                                     C; Accession: JH0564
                                                                                                                                                                                                                                                                                                                                                                                                                          calcium channel alpha-1D chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF--
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                       transmembrane #status predicted
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17.9%;
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                         <IS1>
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F;236-254/Domain: t
F;274-293/Domain: t
F;382-406/Domain: t
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                                                          405 --- IYFVLWWLVSSVIWVNLFLALILEN 429
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                                                                                                                                                                                      APANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK--
                                                                                                                                                                                                                                                                                                            IIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSL
                                                                                                                                                                                                                                                                                                                                                                       VSLFNRFDCFVVCGGITETILVELEIMSPLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                     -----WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRMLNMLIVFRFLR 290
                                                                                                                                                                                                                                                    IFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 190; DB 2;
Pred. No. 6.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted
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<113>
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<IS4>
<IS5>
<IS6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <S51>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                ---ISVFRCVRLLR
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Gaps

20;

R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits

Schwarz, 24 - Nov - 1999

from the

marine ray

O

C;Species: Discopyge ommata
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change

calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge

ommat

347 625

676

240

C; Accession: A47447

RESULT A47447

Matches

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A;Gene: TuCal
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium binding; calcium channel
                                                                                                                                                                              A:Molecule type: mRNA
A:Residues: 1-2262 <OKA>
A:Cross-references: EMBL:AB013604; PIDN:BAA34927.1
                                                                                                                                                                                                                                                                                                                 R:Okamura, Y.; Okagaki, R. submitted to the EMBL Data Library, May 1998 A;Description: TuCal, ascidian calcium channel alphal-subunit.
                                                                                                                                         A:Experimental source: young tadpole larvae C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                          calcium channel alphal-chain - sea squirt (Halocynthia roretzi)
N;Alternate names: ascidian calcium channel alphal-subunit
C;Species: Halocynthia roretzi
C;Date: 22-oct-1999 #sequence_revision 22-oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                        A; Accession: T30890
                                                                                                                                                                                                                                                                                                            A; Reference number: Z20924
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C; Superfamily: voltage-dependent calcium channel protein alpha-1 chain
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    Best Local Similarity
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A47447; MUID:93248175
A;Accession: A47447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                722 NAQELTKEEQE---EEEAINQKHALQKAKEVSPMSAPGFPSTEREFRRHKHMSIWEAR 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 HKWDPRSHLQPLAGTPEATYQMTVELLFRDI--LEEPGEDELTERLSQHPH--LWLCR 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 ITVFQILTGEDWNEVMYNGIKSQGGVNSGMWSSVYFIVLTLFGNYTLLNVFLAIAVDNLA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 VTLWNLMVVNNW-QVFLDAYRRY----SGPWSKIYFVLWWLVSSVIWVNLFLALILENFL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    622 FLLFLFIVVFALLGMQLFGG------QFNFEEGTPP-----TNFDTFPAAI 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 VVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAAL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 IIGSIFDVVWTIIRPETSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLL 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 MVGLL--SLWDMTRM-----LNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGIL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 NFLYYAEFTFLGLFS--SEMFLKMYGCGPR-------LYFHSSFNCFDCGV 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 EEVMLLEENKNAGEKSAL-HVLRRATIKKGRMEMIQTESSEDQYTEISSVG--SPLARAS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 FEVL----SSMYGEGGAFPQATRRG--PSTSLRFCRAPSSSSATTTLTTWGTSSP----- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 FIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRSFLKLRRQQQIERELNGYRAWIDKA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 FIVFTVIGSLFLMNLLTAIIYSQF------RGYLMKSLQTSLFRRRLGTRA----A 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 CRFCSQQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYA-----IF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKSTKLLEGSSYERRKERMLRISIRHMVKSHAFYWIYLGLVALNTVCVAVVHYDQPLWLS 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSYWIGPNDG-----ITQFDNILFALLTVFQCITMEGWTTIL---YNTDDALGAMWNWLY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
  7.2%;
20.2%;
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19.9%; Pred. No. 6.9
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Score 189.5; DE Pred. No. 7e-07;
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              DB 2; Length 2262;
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A;Residues: 1-2270 <WIL>
A;Cross_references: GB:L29385; NID:g495869; pIDN:AAA59205.1; PID:g495870
A;Cross_references: GB:L29385; NID:g495869; pIDN:AAA59205.1; PID:g495870
                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A54972

R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; J. Biol. Chem. 269, 22347-22357, 1994

A;Title: Structure and functional characterization of neuronal alpha-1E calcium chann A;Reference number: A54972; MUID:94350992

A;Accession: A54972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Homo sapiens (man)
C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
A54972
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                                                                                                                                                                                                                                                                                                                                                                              Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
        193 W-----QTWCPFACS----
                                              376 IERELNGYRAWIDKAEEVM-----LAEENKNAGTSALEVLRRATIKRSRTEAMTRDSSDE 430
                                                                                              133 LFRRRLGTRAAFEVLSSMYGEGGAFPQATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSP 192
                                                                                                                                                  316 YNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRAFMKLRRQQQ 375
                                                                                                                                                                                                                                                      259 LEGFDPPHPCGVQGCPAGYECKDWIGPNDGITQFDNILFAVLTVFQCITMEGWTTVL--- 315
                                                                                                                                                                                                   88 YSKNRAYA-----IFFIVETVIGSLELMNLLTAIIYSQF------RGYLMKSLQTS 132
                                                                                                                                                                                                                                                                                                       32 LWGGDPVVPWSCRFCSQQDDGQD----RERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          788 LNVFLAIAVDN 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 VNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              728 IRSNFDTFLQALLTVFQILTGEDWNVVMYNGIEAYGGASTIGLLTSVYFIVLFIGGNYIL 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 WANNFDDFAAALVTLWNLMVVNNWQVF----LDAYRRYS--GPWSKIYFVLWWLVSSVIW 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 LYQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 626 FYSLFNRFDCFYYCGGIVELYLTSSKIMEPLGISVLRCVRLLRIFKMTSSWNSLSNLVAS 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        686 LLNSIRSIASLLVLLFLFIIIFALLGMQMFGGRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 -VGLLSLWD-------MTRM------LIMILIVFRFLRIIPSMKPMAVVASTVLG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 GFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCWRPEM------ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 ETWWQMQRRALFKVCYSRRWRRWNRKTRRRCRTMVKSKSFYWLVIVLVFCNTLSLATEHY 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 TTWGT-----SSPWQTW-----CPF---ACSWCWNQM----CCLLSVMTSSW 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 EFQKLREKQQTDEDMKGYMDWTTQAEDLDPMNDEDREDRRSASNEQLNDADSEVSGLQID 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AFEVL-----SSMYGEGGAFPQATRRGP-----STSLRFCRAPSSSSATTTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 YYMNDAVGNLWPWIYFVSLIIIGSFFVMNLILGVLSGEF-----SKEREKANARG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 WG-----RHCSGGMICESDWAGPSKGIINFDTFYFAVITVFQCITMEGWTDVL--- 418
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 YSKNRAYA----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 WGGDPVVPWSCRFCS-----QQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ROPPWL-----TLAQDLANKILLTLFTIEMLVKMYSLGMQQY 625
                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 189; DB 2;
19.4%; Pred. No. 7.7e-07;
ative 91; Mismatches 218
----WCWMQMCCLLSV--MTSS----WGFSTASSLCT 229
                                                                                                                                                                                                                                                                                                                                                                      Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 2270;
                                                                                                                                                                                                                                                                                                                                                           Indels 132; Gaps
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QY 88 YSKNRAYAIFFIVETVIGSLELMNLLTAIIYSQF	A;Accession: S29237 A;Accession: S29247 A;Accession: CAAA8041.1; PID: S1475 A;Accession: S29247 A;Accession: S29247 A;Accession: CAAA8041.1; PID: S1475 A;Accession: CAAA8041.1; PID: CAAA8041.1; PID: CAA	707 707 472 472 767 12 12 13 12 13 14 12 15 16 16 16 16 16 16 16 16 16 16 16 16 16	Db 431 HCVDISSYGTPLARASIKSAKVDGVSYFRHKERLLRISIRHMVKSQVFYWIVLSLVALNT 490 Qy 230 TCWSCCSRSLP-WACE
Db 430	32 LWGGDPVPWSCRE	calcium C.Spec C.Spec C.Date C.Acces R.Nicker R.Nicker A.Fiti A.Fete A.Facces A.Fote A	Qy 304 TVLGLVQNMRAFGGILVVVYYVFALIGINLFRGVIVALPGNSSLAPANGSAPCGSFE 360 1

A;Cross-references: GB:X05921; NID:g1547; PIDN:CAA29355.1; PID:g1548 C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain C;Keywords: phosphoprotein; transmembrane protein

19;

A; Molecule type: mRNA A; Residues: 1-1873 <TAN>

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dihydropyridine receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
C;Accession: A30063
R;Tanabe, T; Takeshima, H.; Mikami, A.; Flockerzi, V.; Takahashi, H.; Kangawa, K.; Koj:
                                                                                                                                                                                                                     RESULT 15
A30063
     Nature 328, 313-318, 1987
A; Title: Primary structure of the receptor for calcium channel blockers from skeletal mu. A; Reference number: A30063; MUID:87258269
A; Accession: A30063
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A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel A;Reference number: A54972; MUID:94350992
A;Recession: B54972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L29384; NID:g495867; PIDN:AAA59204.1; PID:g495868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     voltage-dependent calcium channel alpha 1E-1 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-2251 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Species: Homo sapiens (man)
;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
;Accession: B54972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                        647
                                                                                                                                                                                                                                                                                                                                                          376 LVTLWNLMVVNNW-QVFLDAYRRY----SGPWSKIYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 VTVGSIFEVVWAIFRPGTSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 LFRRRLGTRAAFEVLSSMYGEGGAFPQATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 YNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRAFMKLRRQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 LEGFDPPHPCGVQGCPAGYECKDWIGPNDGITQFDNILFAVLTVFQCITMEGWTTVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       752 RRHHMSMWEPRSSHLRERRRH 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 YSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQF-----RGYLMKSLQTS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 LWGGDPVVPWSCRFCSQQDDGQD----RERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                           IMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWSAIYFIVLTLFGNYTLLNVFLAIAVDN 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVVVY----YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IERELNGYRAWIDKAEEVM-----LAEENKNAGTSALEVLRRATIKRSRTEAMTRDSSDE
                                                                                                                                                                                                                                                                                                                                                                                                                LFLLFIVVFALLGMQLFGGRFNFNDGTPSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMVGLL--SLWDMTRM-----LNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACVAIVHHNQPQWLTHLLYYAEFLFLGLFLLEMSLKMYGMGPR----LYFHSSFNCFDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCVDISSVGTPLARASIKSAKVDGVSYFRHKERLLRISIRHMVKSQVFYWIVLSLVALNT
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YTLLNVFLATAVDNLANAQELTKDEQEEEEAFNQKHALQKAKEVSPMSAPNVPSIERDRR 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%; Score 186.5; DB 2
20.5%; Pred. No. 1.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GTCPTPATCLTGSSPLSCWR-P
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                                   441 QPLAGTPEATYQMTVELLFRDILEEPGEDELTERLSQHP 479
                                                                           625 MAYGGPSYPGVLVCIYFIILFVCGNYILLNVFLAIAVDNLAEAESLISAQKAKAEERKRR 684
                                                                                                                                                                                           337 VIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNW-QVFLDAY 395
                                                                                                                                                                                                                                                                                 280
                                                                                                                                                                                                                                                                                                                  491 YEMSIFUREDCEVVCSGILELLLVESGAMTP----LGISVLRC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389
                                                                                                                                                                                                                                                                                                                                                                                                                                             203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 VLGVLSGEFTKEREKAKSRGTFQKLREKQQLEEDLRGYMSWITQGEVMDVEDLREGKLSL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 LTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 ITHFDNFGFSMLTVYQCITMEGWTDVL---YWVNDAIGNEWPWIYFVTLILLGSFFILNL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 LTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYA----IFFIVFTVIGSLFLMNL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
    KMSRGLPDKT----
                                                                                                              RRYSGPWSK-----IYFVLWWLVSSVIWVNLFLALILENFLH------KWDPRSHL 440
                                                                                                                                                                                                                                                                           LNMLIVFRELRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRG 336
                                                                                                                                                                                                                                                                                                                                                                                               SRVFYWLVILIVALNTLSIASEHHNQPLWLTHLQDIANRVLLSLFTIEMLLKMYGLGLRQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                         ---WCWMQMC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEGGSDTESLYEIEGLNKIIQFIR------
                                                                                                                                                                                                                                   -----IRLLRLFKITKYWTSLSNLVASLLNSIRSIASLLLLLFLFIIIFALLGMQLFGG
                                                                                                                                                                                                                                                                                                                                                        SLCT----TCWSCCSRSLP-WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRM 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EGGAFPQATR---RGPSTSLRFCRAPSSSSATTTLTTWGTSSPWQTW----CPFACS---- 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%; Score 186; DB 2; 18.1%; Pred. No. 1.1e-06;
                                                                                                                                                          -----DFEDTEVRRSNFDNFPQALISVFQVLTGEDWNSVMYNGI 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
-EEEKSVMAKKLEQKP 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     ----CLLSVMT----SSWGFSTAS 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178;
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OM protein - protein search, using sw model
                                                             Run on:
October 8, 2002, 09:08:41; Search time 25 Seconds (without alignments) 751.159 Million cell updates/sec
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Title: Perfect score: US-09-918-359-7 2634

Sequence: 1 MSSACWEATGRCRLGGGWMV......PGEDELTERLSQHPHLWLCR 485

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13 14 15 16 16 17 19 19 20 20 20 20 20 20 20 20 20 20 20 20 20	11 55 54 44 11 11 12	Result No.
184 184 179.5 178.5 178.5 177.175.5 175.5 175.5 175.5 175.5 175.5 179.5 169.5 169.5 163.5 163.5 163.5 163.5 163.5 163.5	200 196 194 194 194 191 190 189.5 187.5 187.5 187	Score
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22273 22339 22133 22133 22133 22133 2333 2353 2354 22505 2355 2350	2190 2169 2269 2272 2272 2312 1610 2223 1966 2166 2159 2259 1873	Length I
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Q13698 nomo Sapien Q13936 homo Sapien Q13936 homo Sapien Q05152 oryctolagus P15381 oryctolagus P27732 rattus norv Q01815 mus musculu Q00975 homo Sapien Q95180 homo Sapien Q95180 homo Sapien Q95098 rattus norv Q01855 homo Sapien Q92098 rattus norv Q01855 homo Sapien Q92098 rattus norv P97445 mus musculu Q55017 mus musculu Q55017 mus musculu P54282 rattus norv P94486 oryctolagus Q25452 musca domes P22316 cyprinus ca P54287 rattus norv Q9ny46 homo sapien P15389 rattus norv Q9ny46 homo sapien P15389 rattus norv	gall ratturatturatturatturatturatturatturatt	Description

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ALIGNMENTS

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Ionic channel; Transmembrane; Ion transport; Voltage-gacalcium channel; Glycoprotein; Repeat; Multigene family Calcium-binding; Phosphorylation; Alternative splicing.

REPEAT 108 404 II.

REPEAT 530 776 II.

REPEAT 894 1176 III.

REPEAT 1213 1496 TV
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N-LINKED (GLCNAC. ...) (POTENTIAL).
MISSING (IN ISOFORM I-II-LOOP).
ILGYADYVETSHETEZILK -> ILGYEDYAFTAIFTVEI
LLK (IN ISOFORM IIIS2).
MISSING (IN ISOFORM IVS2-IVS3).
GYFSDAWNTFDSLIVIGSIVDVLJSEAD -> HYFTDAWNT
FDALITVGSVVDIAITEVN (IN ISOFORM IVS3).
AGLRTILHDIGFEIRRAISCDLQDDEPEENNPDEEE -> VL
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CALCIUM ION SELECTIVITY AND PERMEABILI
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CALCIUM ION SELECTIVITY AND PERMEABILI
(BY SIMILARITY).
TO DIHYDROPYRIDINES (BY SIMILARITY).
TO DHYDROPYRIDINES (BY SIMILARITY).
TO PHENYLALKYLAMINES (BY SIMILARITY).
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Pred. No. 9.1e-08
7; Mismatches 16
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MISSING (IN CLONE PSE29/31-2).

RNGALFGNHIMHISSDRRD -> VMSEHGYVIFLLCNMSFI
E (IN CLONE PSE29/31-1).

MISSING (IN CLONE PSE29/31-1).
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MISSING (IN CLONE PSE48/154-1).
MW; 10680C1CB7708651 CRC64;
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CALCIUM ION SELECTIVITY AND PERMEABILITY
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MEDLINE-93374932; PubMed-8396138; Hell J.W., Yokoyama C.T., Wong S. Catterall W.A.;
                                                                                                                                           Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.; "Multiple calcium channel transcripts in rat osteosarcoma cells: selective activation of alpha 1D isoform by parathyroid hormone."; Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).
                                                                                            PHOSPHORYLATION
                                                                                                                                                                                                                                                                  TISSUE=Osteosarcoma;
MEDLINE=96074617; PubMed=7479909;
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1202-1495 FROM N.A. (ISOFORM DELETED D1 FORM/ROB2).
                                                                                                                                                                                                                                                                                                                                                                                                   Tezuka N., Ali M., Chwalisz K., Garfield R.E.; "Changes in transcripts encoding calcium channel subunits of rat myometrium during pregnancy."; myometrium during pregnancy."; am. J. Physiol. 269:C1008-C1017(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Myometrium;
MEDLINE=96043375; PubMed=7485440;
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O1-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
voltage-dependent L-type calcium channel alpha-1C subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle) (RBC).
CACNALC OR CACNLIA1 OR CCHLIA1 OR CACH2 OR CACN2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91299339; PubMed-1648941;
Snutch T.P., Tomlinson W.J., Leonard J.P., Gilbert M.M.;
"Distinct calcium channels are generated by alternative ;
are differentially expressed in the mammalian CNS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koch W.J., Ellinor P.T., Schwartz A.; "cDNA cloning of a dihydropyridine-sensitive calcium channel from rat aorta. Evidence for the existence of alternatively spliced forms.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al subunit generates developmentally regulated isoforms in the rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92159076; PubMed=1311102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1269-1415 FROM N.A. (ISOFORMS S3A; S3B AND DELETED D1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90239020; PubMed=1692134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutually exclusive exon splicing of the cardiac calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1168-1413 FROM N.A.
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                          Wong S.T.,
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                       Warner C.,
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                       Snutch T.P.
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"Differential phosphorylation of two size forms of the neuronal class C L-type calcium channel alpha 1 subunit.";

J. Biol. Chem. 268:19451-19457(1993).

-1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: EXPRESSED FROM EMBRYONIC DAY 16 THROUGHT THE
                                                                                                                                                                                                                                                                     ADULT:

ADULT:

ADULT:

ADULT:

DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4): S4 SEGMENTS
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTIF
INHIBITS THE OPENING OF THE CHANNEL (BY SIMILARTY).

PTM: PHOSPHORYLATION BY CAPK ACTIVATES THE CHANNEL (PROBABLE). IS
ALSO PHOSPHORYLATED IN VITRO BY CAM-KINASE II, PKC AND CGPK.

SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
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Calcium channel; Glycoprotein; Repeat; Multigene family; Calcium-binding; Phosphorylation; Alternative splicing. REPEAT 141 438 I. EMBL; Pfam; PF00520; ion_trans; 4. PRINTS; PR00167; CACHANNEL. EMBL; InterPro; Ionic channel; InterPro; InterPro; M89924; AAA41460.1; M91241; AAA41460.1; S80558; AAB35528.1; U31815; AAA89157.1; IPR002077; Ca_channel_TrpL.
IPR002111; Cat_channel_TrpL.
IPR000636; Cation_chan_non_lig.
IPR001692; Channel_pore_Ca_Na. Transmembrane; Ion transport; Voltage-gated channel; JOINED.

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CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

CALCIUM ION SELECTIVITY AND PERMEABILITY
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$2 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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$5 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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$7 OF REPEAT IV (POTENTIAL).

$1 OF REPEAT IV (POTENTIAL).
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$4 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$5 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

$6 OF REPEAT I (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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S2 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT I (POTENTIAL).
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S6 OF REPEAT IV (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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S5 OF REPEAT IV (POTENTIAL).
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
voltage-dependent R-type calcium channel alpha-1E subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 6) (RBE-II) (RBE2)
(Brain calcium channel II) (BII).
CACNALE OR CACNALA6 OR CACH6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain; MEDLINE=93262464; PubMed=8388125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 LYIFGSFFYLNLYLGYLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDI 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soong T.W., Stea A., Hodson C.D., Dubel S.J., Vincent S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure and functional expression of a member of the low voltage-
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Pfam; PF00520; ion_trans; 4.

PRINTS; PR00167; CACHANNEL.

Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

Ionic channel; Glycoprotein; Repeat; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
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       EXTRACELULAR (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

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S1 OF REPEAT III (POTENTIAL).
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S2 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT I (POTENTIAL).
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S6 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT II (POTENTIAL).
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S4 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT I (POTENTIAL).
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OVELDAYRY?SGPWS : : EVMYNGIRSQGGVSSGMWS	SFG FRG	SSPWOTWCPFACSW:	tch 7.4%; al Similarity 20.8%; 113; Conservative 86 LWGGDPVVPWSCRFCSQQDDGQD-	1467 1485 1493 1512 1513 1561 1561 1650 1676 2222 672 704 704 723 1064 1183 2196 608 1324 1615 388 1324 1615 388 1518 388 1518
YRKY:SGPWSKIYFVLWMLVSSVIWVNLFLALILENFL 431	IFKITKYWASLRNLVVSLMSSMKSIISLLELLE 56 APANGSAPCGSFEQLEYWANNFDDFAAALVTLW 38 III	-WGESTASSICTTCWSC 23 -WGIVLSVVALNITACVAI 44 YWIVLSVVALNITACVAI 42 TGSSPLSCWR-PEMVGL 27 ; ; ;	Score 194; DB 1; Lei Pred. No. 2.7e-07; 6; Mismatches 221; RERLTYFQNLPESLTSLL' : : : : : : WIGDNDGITQFDNILFAVLTVE SLFLMNLLTAIIYSQF : : : : : : : : SFFVLNTLYLGVLSGEFAKERER' MVGEGGAFPQATRRGPSTSLR- MVGEGGAFPQATRRGPSTSLR-	EXTRACELLULAR (POTENTIAL). \$2 OF REPEAT IV (POTENTIAL). CYTOPLASMIC (POTENTIAL). \$3 OF REPEAT IV (POTENTIAL). \$3 OF REPEAT IV (POTENTIAL). \$4 OF REPEAT IV (POTENTIAL). \$5 OF REPEAT IV (POTENTIAL). CYTOPLASMIC (POTENTIAL). POLY-ARG. POLY

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CCACADIA MADDIN RX MEDLIN 
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                                                                                                                                                                                 J. BIOL. Chem. 269:22347-22357(1994).

J. BIOL. Chem. 269:22347-22357(1994).

IF FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM INOS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM—DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BY OMEGA-AGATOXIN-ITIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIOINES (DHP), OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IIIA). THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.

IN A 1:1:11 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1, SUBUNIT SUBUNIT IS SUBUNIT IS SUBUNIT IS SUBUNIT OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:11 RATIO. THE AUXILLARY SUBUNITS BETA AND ALPHA-2/DELTA CHANNEL ACTIVITY. THE AUXILLARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISCLIPIDE BRIDGE REGILATE THE CHANNEL ACTIVITY.

SUBCELLULAR LOCATION: Integral membrane protein.

INDEACH SYNTHE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE PROBABLY REPRESENT THE COLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4), S4 SEGMENTS PROBABLY REPRESENT THE CALCIUM CHANNEL ALPHA-1 SUBUNITS.

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BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS

FAMILY.
                                                This SWISS-PROT entry is copyright. It is produced through a obetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calcium channel subtypes.", J. Biol. Chem. 269:22347-2: -!- FUNCTION: VOLTAGE-SENS!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C; TISSUE-Brain; MEDLINE-94350992; PubMed-8071363;
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MGI:106217; Cacnale.
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Rodentia;
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                                                                    (See http://www.isb-sib.ch/announce/
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prro; IPR002111; Cat_channel_TrpL.
prro; IPR000636; Cation_chan_non_lig.
prro; IPR001682; Channel_pore_Ca_Na.
prf00520; ion_trans: 4
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                                                         EXTRACELLULAR (POTENTIAL).

S6 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S1 OF REPEAT III (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
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$2 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$3 OF REPEAT II (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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S1 OF REPEAT II (POTENTIAL).
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S5 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S6 OF REPEAT I (POTENTIAL).
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S4 OF REPEAT I (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL).
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S2 OF REPEAT I (POTENTIAL).
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S1 OF REPEAT I (POTENTIAL).
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$6 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
$1 OF REPEAT IV (POTENTIAL).
                     POLY-ARG.
BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY
                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT IV (POTENTIA
EXTRACELLULAR (POTENTIAL)
S6 OF REPEAT IV (POTENTIA
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S5 OF REPEAT III (POTEN
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S4 OF REPEAT IV (POTENTIAL).
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S2 OF REPEAT IV (POTENTIAL).
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S4 OF REPEAT III (POTENTIAL)
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Repeat; Multigene family;
         SIMILARITY).
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ID CCAE_HUMAN
AC Q15878; Q14:
DT 15-JUL-1999
DT 15-JUL-1999
DT 16-CCT-2001
DE VOLtage-depute channel II)
DE Channel II)
GN CACNAIE OR (OS HOMO Sapien)
OC Eukaryota; E
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Best Local
                               Q15878; Q14581; Q14580;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-UL-1999 (Rel. 40, Last annotation update)
Voltage-dependent R-type calcium channel alpha-1E subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 6) (Brain calcium Channel II) (BII).
CACNA1E OR CACNLIA6 OR CACH6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA_BIND
MOD_RES
CA_BIND
CARBOHYD
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                      RH
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                                                                                                                                                                                                                                                                         LTKDEQEEEEAFNQKHALQKAKEVSPMSAPNMPSIERDRRRRHHMSMWEPRSSHLRERRR
                                                                                                                                                                                                                                                                                                                           QILTGEDWNEVMYNGIRSQGGVSSGMWSAIYFIVLTLFGNYTLLNVFLAIAVDNLANAQE
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                                                                                                                                                                                                                                                                                                                                                                                 LFIVVFALLGMQLFGGRFNFNDGTPSA--
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                                                                                                                                                 STANDARD;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
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CALCIUM ION SELECTIVITY AND
 Craniata; V
Catarrhini;
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BY SIMILARITY
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CALCIUM ION SELECTIVITY
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            Vertebrata;
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 Hominidae;
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           Euteleostomi
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RA WILLIAMS M.E., MATUBLO L.M., Deal C.R., Hans M., Brust P.E.,
RA Philipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
RA Philipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
RT "Structure and functional characterization of neuronal alpha in calcium channel subtypes.";
RT J. Biol. Chem. 269:22347-22357(1994).

CC IN A VARIETY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED CC. IN A VARIETY OF CALCIUM CERCIPANSMITTER RELEASE, GENE EXPRESSION.
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E CC.
CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
CC GELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E CC.
CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HYA) GROUP AND ARE BLOCKED DY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-TIVA (OMEGA-CAA-TIIA).
CC THEY ARE HOMEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-CAA-TIIA).
CC THEY ARE HOMEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-CAA-TIIA).
CC IMPORTANT FOR INFORMATION OF FIRING PATTERNS OF NEURONS WHICH IS SUBUNIT: VOLTAGE-SENSITIVE ALCIUM CHANNELS CONTAINED ARE MICCYED BE COULTAGE.
CC INFORMINE AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUBVITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUBVITIVE ALPHA-1 SUBUNITS. BETA AND DELTA SUBUNITS COUNTING THE CHANNEL ACTIVITY BETA AND ALPHA-2/DELTA COUNTING SUBVITIVE ALPHA-1 SUBUNITS. BETA AND ALPHA-2/DELTA COUNTING SUBVITIVE ALPHA-1 SUBVITIS BETA AND ALPHA-2/DELTA COUNTING SUBVITIVE ALPHA-1 SUBVITIS BETA AND ALPHA-2/DELTA COUNTING SUBVITIS BETA AND ALPHA-2/DELTA COUNTING SUBVITIS BETA AND ALPHA-2/DELTA COUNTING SUBVITIS BETA AND ALPHA-1/CHANNEL ACTIVITY.
CC INFORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBVITIS BETA AND ALPHA-1/CHANNEL ACTIVITY.
CC INFORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBVITIS BETA AND ALPHA-1/CHANNEL ACTIVITY.
CC INFORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBVITIS BETA AND ALPHA-1/CHANNEL ALPHA-1 SUBVITIS BETA AND ALPHA-1/
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Interro; A. Prontans; 4.

Pfam; PF00520; ion_trans; 4.

PRINTS; PR00167; CACHANNEL.

Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

Tonic channel; Glycoprotein; Repeat; Multigene family; EMBL; This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and EMBL; InterPro; IPR002077; Ca_channel.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR0001682; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na. EMBL; L27745; or send an email to license@isb-sib.ch). entities requires a license agreement 601013; L27745; AAA72125.1; L29384; AAA59204.1; L29385; AAA59205.1; noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/ restrictions on and TEMBL ST þ collaboration 'n no way

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$4 OF REPEAT I.

CYTOPLASMIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

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099244; 099245;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Voltage-dependent L-type calcium channel alpha-1D subunit channel, L type, alpha-1 polypeptide isoform 2).
CACNAID OR CACNLIA2 OR CCHILA2 OR CACH3 OR CACN4.
                     Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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MISSING (IN REF. 2).
R -> P (IN REF. 2).
G -> R (IN REF. 2).
C -> W (IN REF. 2).
S -> R (IN REF. 2).
S -> V (IN REF. 2).
G -> V (IN REF. 2).
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MISSING (IN ISOFORM ALPHA-1E-1).
I -> M (IN REF 2).
WP -> LAL (IN REF, 2).
T -> A (IN REF, 2).
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Pred. No. 4.
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PART REPRESENTATION OF STREET TO SOLVE THE PROPERTY OF SOLVE THE P
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11 SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNIT IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

1-1 SUBCELLULAR LOCATION: INTEGTAL membrane protein.

1-1 ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; HCA3A (SHOWN HERE), CACH3B AND CACH3D; ARE PRODUCED BY ALTERNATIVE SPLICING. CACH3B IS IDENTICAL TO HCA3A IN THE FRAGMENT SEQUENCED.

1-1 TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART AND SKELETAL MUSCLE.

1-1 DOMAIN: EACH OF THE FOUR INVERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (51), S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (54). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

1-1 SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
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-I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARLETY OF CALCIUM-DEPENDENT PROCESSES, ICLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOMEVER INSENSITIVE TO OMEGA-CONOTOXIN-TUTN (AUGUSTA) AND OMEGA-TOXAGA-TVAN
                                                                                                                                            REPEAT
                                                                                                                                                                               Calcium channel; Glycoprotein; Rej
Calcium-binding; Phosphorylation;
REPEAT 112 408 I.
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002077; Ca_channel_TrpL.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
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EMBL; M57970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a
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"Molecular diversity of L-type calcium channels. Evidence for alternative splicing of the transcripts of three non-allelic J. Biol. Chem. 265:20430-20436(1990).
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                                                                             REPEAT
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                                                                                                                                                                                                                                                                                 lonic channel;
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00520;
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                                                                                                                                                                                                                                                                                                             PR00167; CACHANNE
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AAA62807.1; -.
                                                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                                                                                                                                                    CACHANNEL.
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CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT I (POTENTIAL).
                                                                                                                                                                                                Ion transport; Voltage-gated channel; Repeat; Multigene family; ion; Alternative splicing.
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154 224 328 338 1303	1163 1484 1473 1473 1502	1404	70	363	836 445	5 6	1437 1462 1610	1370	1331	1286	1257	1222	1146 1203	1035 1125	1015	976	951 970	939	903	751 987	672 726	632 651	613	584	557 576	542	405 500	380	272	253 253	213	182 194	162
N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). SYFSDAWNTFDSLIVIGSIIDVALSEADPTESESIDLPTAT PG -> HYFTDAWNTFDALIVVGSVVDIAITEVN (IN ISOFORM CACH3D). MW; B3B2E3794D936F79 CRC64;	O DIHYDROPYRIDINES (BY SIMILARI O DIHYDROPYRIDINES (BY SIMILARI O PHENYLALKYLAMINES (BY SIMILARI HOSPHORYLATION (BY CAPK) (POTEN OTENTIAL.	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY). CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY)	ION SELECTIVITY AND P	SIMILARITY). CALCIUM ION SELECTIVITY AND PERMEABILITY	POLY-LEU. POLY-GLU. BINDING TO THE BETA SUBUNIT (BY	POLY-MET.	EXTRACELLULAR (POTENTIAL). S6 OF REPEAT IV (POTENTIAL). CYTODIASMIC POTENTIAL).	S5 OF REPEAT IV (POTENTIAL).	EXTRACELLULAR (POTENTIAL). S4 OF REPEAT IV (POTENTIAL).	CYTOPLASMIC (POTENTIAL). S3 OF REPEAT IV (POTENTIAL).	SZ OF REPEAT IV (POTENTIAL).	/ (POTENTIAL	II (POT	S5 OF REPEAT III (POTENTIAL). EXTRACELLULAR (POTENTIAL).	S4 OF REPEAT III (POTENTIAL). CYTOPLASMIC (POTENTIAL).	EXTRACELLULAR (POTENTIAL).	CYTOPLASMIC (POTENTIAL). S3 OF REPEAT III (POTENTIAL).	S2 OF REPEAT III (POTENTIAL).	II (POTENTI	I (POTENTIA	S5 OF REPEAT II (POTENTIAL). EXTRACELLULAR (POTENTIAL).	S4 OF REPEAT II (POTENTIAL). CYTOPLASMIC (POTENTIAL).	SS OF REPEAT II (POTENTIAL). 'EXTRACELLULAR (POTENTIAL).	CYTOPLASMIC (POTENTIAL).	TAL)	REPEAT	6 OF REPEAT	TRACELLUL	YTOPLASMIC (POTENTIAL).	7	3 OF REPEAT I (POTENTIA	YTOPLASMIC (D	(POTENTIAL)

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FSGNGRQCAVNGTECRSGWVGPNGGI-----

6 WEATGR-CRLGG-----GWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLT

60

Matches Query Match Best Local

91;

Conservative

96;

Mismatches

174;

Indels 158;

Gaps

18;

59

Similarity

7.2%; 17.9%;

Score 190; Pred. No.

4e-07 DB 1;

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GVLSGEFSKEREKAKARGDFQKLRENEQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKR

TRRGPSTSLRFCRAPSSSSATTTLTTWGT-----SSPWQTWCPF

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NFDNFAFAMLTVFQCITMEGWTDVL---YWMNDAMGFELPWVYFVSLVIFGSFFVLNLVL YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYA----IFFIVFTVIGSLFLMNLLT

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RC TISSUE-electric lobe;

RX MEDLINE-93248175; pubmed=7683405;

RA HOTNE W.A., Ellinor p.T., Inman I., Zhou M., Tsien R.W., Schwarz T.L.;

RA HOTNE W.A., Ellinor p.T., Inman I., Zhou M., Tsien R.W., Schwarz T.L.;

RY "Molecular diversity of Ca2+ channel alpha 1 subunits from the marine

RT ray Discopyge ommata.";

Proc. Natl. Acad. Sci. U.S.A. 90:3787-3791(1993).

Proc. Natl. Acad. Sci. U.S.A. 90:3787-3791(1993).

C -1- FUNCTION: THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM

CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE

C -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT

C COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS

C FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS

C SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM

C CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA

C LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY (BY
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                          Probable voltage-dependent
                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
30-MAY-2000 (Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAE_DISOM
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002111; Cat_channel
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Pro; IPR000636; Cation_chan_non_lig.
Pro; IPR001682; Channel_pore_Ca_Na.
Pr00500; ion_trans; 4.
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                                                                                   EXTRACELLULAR (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).

S4 OF REPEAT III (POTENTIAL).

S4 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).
                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S4 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).
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S2 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S3 OF REPEAT I (POTENTIAL).

S3 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S4 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT I (POTENTIAL).
      EXTRACELLULAR (POTENTIAL).
$5 OF REPEAT III (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
$1 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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S6 OF REPEAT I (POTENTIAL).
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S1 OF REPEAT I (POTENTIAL).
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; Repeat; Multigene family;
                                                                                                                                                                                                                  LASMIC (POTENTIAL)
REPEAT III (POTENT
                                                                                                                                                                                                                                                (POTENTIAL).
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SIMILARITY).
SUBCELLULAR LOCATION: Integral TISSUE SPECIFICITY: EXPRESSION membrane mbrane protein. HIGHER IN THE FOREBRAIN THAN

THE ELECTRIC LOBE.

DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SECKENT (S4). S4 SECMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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NAQELTKEEQE----EEEAINQKHALQKAKEVSPMSAPGFPSTEREFRRHKHMSIWEAR 776
                   HKWDPRSHLQPLAGTPEATYQMTVELLFRDI--LEEPGEDELTERLSQHPH--LWLCR 485
                                                                                                                                                                                                                                                                                                                                                                          CRFCSQQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYA----IF 97
                                                                                     FLLFLFIVVFALLGMQLFGG------QFNFEEGTPP-----TNFDTFPAAI
                                                                                                          VVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAAL
                                                                                                                                                     MVGLL--SLWDMTRM-----LNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGIL
                                                                                                                                                                                                MCCLLSVMTSSWGFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCWR-PE
                                                                                                                                                                                                                                                                 EEVMLLEENKNAGEKSAL-HVLRRATIKKGRMEMIQTESSEDQYTEISSVG--SPLARAS
                                                                                                                                                                                                                                                                                          FEVL---
                                                                                                                                                                                                                                                                                                            FIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRSFLKLRRQQQIERELNGYRAWIDKA
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                                                                                                                              IIGSIFDVVWTIIRPETSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLL
                                                                                                                                                                           NFLYYAEFTFLGLES--SEMFLKMYGCGPR------LYFHSSFNCFDCGV
                                          ITVFQILTGEDWNEVMYNGIKSQGGVNSGMWSSVYFIVLTLFGNYTLLNVFLAIAVDNLA
                                                              VTLWNLMYVNNW-QVFLDAYRRY----SGPWSKIYFVLWWLVSSVIWVNLFLALILENFL 431
                                                                                                                                                                                                                                                                                                                                  FIVFTVIGSLFLMNLLTAIIYSQF-------RGYLMKSLQTSLFRRRLGTRA----A 143
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$4 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$5 OF REPEAT IV (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

$6 OF REPEAT IV (POTENTIAL).

$6 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCN/
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Pred. No. 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
PHOSPHORYLATION (BY
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CALCIUM ION SELECTIVITY
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S3 OF REPEAT IV (POTENTIAL).
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RESULT 8

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RI A GENOMICS 45:340-347(1997).

RI GENOMICS 45:340-347(1997).

RI GENOMICS 45:340-347(1997).

CC :- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE CC: PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1F CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1F CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1F CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-RASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)

CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)

CC PHENYLALKYLAMINES, BENZONTHIZEPINES, AND BY OMEGA-AGA-TUA).

CC (HANGEA-CTM-GULA) AND OMEGA-AGA-TOXIN-TUA (OMEGA-AGA-TUA).

CC (HANGEA-CTM-GULA) AND OMEGA-AGA-TUA).

CC (HANGEA-CTM-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   060840; 043901;
15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
16-OCT-2001 (Rel. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D'Urso M.,
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Nat. Genet. 19:260-263(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strom T.M., Nyakatura G., Apfelstedt-Sylla E., Lorenz B., Weber B.H.F., Wutz K., Gutwillinger Drescher B., Sauer C., Zrenner E., Meitinger T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Voltage-dependent L-type calcium channel alpha-1F subunit CACNA1F OR CACNAF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence-based exon prediction around the synaptophysin locus reveals gene-rich area containing novel genes in human proximal Xp.";
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                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
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38, Last sequence update)
40, Last annotation update)
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Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family; Calcium-binding; Phosphorylation; Disease mutation; Vision.
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InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
Pfam; PF00520; ion_trans; 4.
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AJ224874;
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EXTRACELLULAR (POTENTIAL).

$4 OF REPEAT II (POTENTIAL).

$5 OF REPEAT II (POTENTIAL).

$5 OF REPEAT II (POTENTIAL).

$5 OF REPEAT II (POTENTIAL).

$6 OF REPEAT III (POTENTIAL).

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$7 OF REPEAT III (POTENTIAL).

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$3 OF REPEAT III (POTENTIAL).

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$4 OF REPEAT III (POTENTIAL).

$5 OF REPEAT IV (POTENTIAL).

$2 OF REPEAT IV (POTENTIAL).

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$3 OF REPEAT IV (POTENTIAL).

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$5 OF REPEAT IV (POTENTIAL).
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CYTOPLASNIC (POTENTIAL).

S3 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S4 OF REPEAT I (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

S5 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S6 OF REPEAT II (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

S1 OF REPEAT II (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

CYTOPLASNIC (POTENTIAL).
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IV.
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT I (POTENTIAL).
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     QALLTVFQILTGEDWNYVMYDGIMAYGGPFFPGMLVCIYFIILFICGNYILLNVFLAIAV
                                    AALVTLWNLMVVNNWQVFL-DAYRRYSGPWSK----IYFVLWWLVSSVIWVNLFLALIL
                                                                      SLLLLEFFIIIFSLLGMQLFGGKF----
                                                                                                      GILVVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFA
                                                                                                                                        MQPLG--
                                                                                                                                                                       SSPLSCWRPEMVGLLSLWDMTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFG
                                                                                                                                                                                                      ANKVLLCLFTVEMLLKLYGLGPSAYVSSFFNRFDCFVVCG------GILETTLVEVGA
                                                                                                                                                                                                                                     CWMQMCCLLSV--MTSSWGFSTASSLCT----TCWSCCSRSLPWACEGTCPTPATCLTG
                                                                                                                                                                                                                                                                                           ------RGPSTSLRF-CRAPSSSSA------
                                                                                                                                                                                                                                                                                                                                          TNRRRGRLRWFSHSTRSTHSTSSHASLPASDTGSMTETQGDEDEEEGALASCTRCLNKIM
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18.68;
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                                                                                                                                        ----ISVLRCVRLLRIFKVTRHWASLSNLVASLLNSMKSIA
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CALCIUM ION SELECTIVITY AND PERMEABILI (BY SIMILARITY).
(BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILI (BY SIMILARITY).
TO DIHYDROPYRIDINES (BY SIMILARITY).
TO DHENYLALKYLAMINES (BY SIMILARITY).
TO PHENYLALKYLAMINES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F -> W (IN CSNB2).

/FTId=VAR 001506.

L -> H (IN CSNB2).

/FTId=VAR 001507.

E -> V (IN REF. 3).

MISSING (IN REF. 3).

MISSING (IN REF. 3).

A -> G (IN REF. 3).

A -> G (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
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G -> D (IN CSNB2).
/FTId=VAR_001504.
R -> Q (IN CSNB2).
/FTId=VAR_001505.
R -> W (IN CSNB2).
                                                                                                                                                                                                                                                                                                                                                                         -----SMV-----GEGGAFPQATR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 187.5; DB 1; Pred. No. 7.8e-07; 3; Mismatches 169;
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POLY-ILE.
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BY SIMILARITY.
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                                                                      - NEDQTHTKRSTEDTEP
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N .. E

749 429

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REL Genomics 27:312-319(1995).

CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE CC -!- SUBUNIT: OF CALCIUM-DEPENDENT PROCESSES; INCLUDING MUSCLE CC CALCIUM, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D CC CALCIUM, CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) CC CALCIUM CHANNELS, BENCOTHIAZBEDINES, LONG-LASTING (I-TYPE) CC CALCIUM CHANNELS, BENCOTHIAZBEDINES, AND BY OMEGA-GATOXIN-IIA COMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-CC COMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-AGA-IVA).

CC COMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-AGA-IVA).

CC COMEGA-AGA-IIIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).

CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND VERSES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS EFTA AND ALPHA-2/DELTA CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -I- SUBCRILIURA LOCATION: TOTAGETAL MEMBERS AND ALPHA-2/DELTA CC -I- SUBCRILIURA LOCATION: TOTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
CCAD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAD_HUMAN STANDARD; PRT; 2161 AA.

Q01668; Q13916; Q13931;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-dependent L-type calcium channel alpha-1D subunit channel, L type, alpha-1 polypeptide, isoform 2).
CACNAID OR CACNLIA2 OR CCHLIA2 OR CACH3 OR CACN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura K., Fujii Y., Seino S., Seino The structures of the human calcium ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (BETA-CELL-TYPE ISOFORM), AND VARIANT NIDDM MEDLINE-96044438; PubMed-7557998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expressed in pancreatic beta cells."; proc. Natl. Acad. Sci. U.S.A. 89:584-588(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pancreatic islets;
MEDLINE=92115705; PubMed=1309948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CACNLIA2) and beta subunit (CACNLB3) genes."; Genomics 27:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bell G.I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (BETA-CELL-TYPE ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure and
           SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; NEURONAL-TYPE (SHOWN HERE) AND BETA-CELL-TYPE; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN PANCREATIC ISLETS AND IN BRAIN,
WHERE IT HAS BEEN SEEN IN HIPPOCAMPUS, BASAL GANGLIA, HABENULA AND
THALAMUS. NO EXPRESSION IN SKELETAL MUSCLE.
DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (SI, 22, S3, S5, S6) AND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ture and functional expression of alpha1, alpha2, and beta ts of a novel human neuronal calcium channel subtype."; 8:71-84(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.E., Feldman D.H., McCue A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masuda K., Li Q., Ihara Y., Kubota A.,
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     TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calcium channel alpha 1 subunit
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, S2, S3, S5
NT (S4). S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R., Velicelebi G.,
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S5, S6) AN
S4 SEGMENTS
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; Homo.
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<del>:</del>
                                                                                                                                                                                                                                                                                                                            PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION. POLYMORPHISM: A CHANGE FROM SEVEN TO EIGHT AGT TRINUCLEOTIDE REPEATS, RESULTING IN AN ADDITIONAL N-TERMINAL METHIONINE, HAS BEEN FOUND IN A PATIENT WITH NON-INSULIN-DEPENDENT DIABETES
                                                                                                                                                                                                                                                                                                                     SIMILARITY:
                                                                                                                                                                                                                                                                                                                         (NIDDM)
                                                                                                                                                                                                                                                                                                                    BELONGS TO THE CALCIUM CHANNEL
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                                                                                                                                                                                                                                                                                                                    SUBUNITS
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EMBL;
                                                                                                                                      EMBL;
Calcium channel; Glycoprotein; Repeat; Multigo Calcium-binding; Phosphorylation; Alternative
                   PRINTS; PRUULO, Ionic channel;
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                                                IPR002077; Ca_channel.
IPR002111; Cat_channel_TrpL.
IPR000638; Cation_chan_non_lig
IPR001682; Channel_pore_Ca_Na.
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           Ion transport; Voltage-gated channel;
; Repeat; Multigene family;
   splicing;
 Polymorphism;
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Best Local
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72 LVILTTANNPDVMIPAYSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLM 126
                                          12
                                                                  Local Similarity
                         CR--SGWVGPNGGI------357
                                         CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 71
                                                          94;
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                                                            Conservative
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18.5%;
                                                           81;
                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S5 OF REPEAT III (POTENTIAL).
S6 OF REPEAT III (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT I (POTENTIAL).
                                                                                           BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT III (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).

S6 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S1 OF REPEAT III (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
S3 OF REPEAT II (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT II (POTENTIAL).
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S1 OF REPEAT II (POTENTIAL).
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S6 OF REPEAT I (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL)
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S2 OF REPEAT I (POTENTIAL)
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S1 OF REPEAT I (POTENTIAL).
                                                                   Score 187; DB 1; pred. No. 9.4e-07;
                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).

$2 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$3 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
S5 OF REPEAT IV (POTENT
                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV (POTENTIAL).
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                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
S6 OF REPEAT IV (POTENTIA
                                                                                                                                               POLY-GLU.
                                                           Mismatches 157;
                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                  (POTENTIAL).
                                                                           Length 2161;
                                                            Indels 176;
                                                             Gaps
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CCAEMANT
ID CCAEMANT
AC 002343; Q02
DT 01-JUL-1993
DT 01-JUL-1993
DT 01-JUL-1993
DT 01-GCT-2001
DE VOLTAGE-dep
DE channel, L
DE channel II)
GN CACNAIE OR
OS OTYCTOLAGUS
OC MAMMMAILS: E
OX NCBL. TAXID-
RP SEQUENCE FR
RC TISSUE-BTAI
RX MIDLINE-923
RA NIIGOME T.
RT FONCTIO
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PEND LUCL. 300:(7-13/1372).

11 FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE COVERACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOSORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DITYDROPYRIDINES (DHP), OMEGA-GONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-CTX-GVIA), CALCIUM CHANNELS CONTANING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.

10 SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS OF NEURONS WHICH IS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. BETA AND ALPHA-2/DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Voltage-dependent R-type calcium channel alpha-1E subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 6) (Brain calcium channel II) (BII).
CACNA1E OR CACNLIA6 OR CACH6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 002343; 002344;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92354772; PubMed=1379552; Nildome T., Kim M.S., Friedrich T., Mori Y.; "Molecular cloning and characterization of a feet which heads".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNTSMPTSETESV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSLQTSLFRRRLGTRAAFEVLSSMVG-------EGG-----AFP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rabbit brain.";
Lett. 308:7-13(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVCIYFIILFICGNYILLNVFLAIAVDN 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IYFVLWWLVSSVIWVNLFLALILEN 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFKVTRHWTSLCNLVASLLNSMKSSASLLLLLELFIIIFSLLGMQLFGGKF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NFDETQTKRSTFDNFPQALLTVFQILTGEDWNAVMYDGIMAYGGPSSSGM 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2259 AA
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                                                                                                                                                                                                                                                                                                                                                                  Calcium channel; Glycoprotein; Rep
Calcium-binding; Phosphorylation;
REPEAT 76 354 I.
                                                                                                                               DOMAIN
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InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR00636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
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                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                               Conic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND CORPUS STRIATUM.

DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMENBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMENBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED ANINO ACIDS AT EVERY THIRD POSITION. SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
SUBCELLULAR LOCATION: Integral membrane protectin.
ALTERNATIVE PRODUCTS: 2 ISOPORMS; BII-1 (SHOWN HERE) AND BII-2;
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ABUNDANT IN THE CEREBRAL CORTEX, HIPPOCAMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $29236; $29230
$29237; $2923
                                                                                                                                                                                                                                                                                                                                                                                               channel;
                                                                                                                                                                                                                                                                                                                                                                                                         PR00167;
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1163
1179
1199
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1263
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531
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558
568
568
506
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205
224
224
327
352
477
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109
127
147
147
159
                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Ion transport; Voltage-gated channel; 1; Glycoprotein; Repeat; Multigene family; 9; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                  ion_trans; 4.
                                                                                                                                                                                                                                                                                                                                                                                                         CACHANNEL
   DI OF REPEAT I.

EXTRACELLULAR (POTENTIAL).

S2 OF REPEAT I.

CYTOPLASMIC (POTENTIAL)

S3 OF REPEAT I.
EXTERGELLULAR (POTENTIAL).

$2 OF REPEAT II.

CYTOPLASMIC (POTENTIAL).

$3 OF REPEAT II.

EXTRACELLULAR (POTENTIAL).

$4 OF REPEAT II.

CYTOPLASMIC (POTENTIAL).

$5 OF REPEAT II.

EXTRACELLULAR (POTENTIAL).

$6 OF REPEAT II.

CYTOPLASMIC (POTENTIAL).

$6 OF REPEAT III.

CYTOPLASMIC (POTENTIAL).

$1 OF REPEAT III.

EXTRACELLULAR (POTENTIAL).

$2 OF REPEAT III.

CYTOPLASMIC (POTENTIAL).

$3 OF REPEAT III.

CYTOPLASMIC (POTENTIAL).

$3 OF REPEAT III.

CYTOPLASMIC (POTENTIAL).

$4 OF REPEAT III.

S7 OF REPEAT III.
                                                                                                                                                                                               S6 OF REPEAT CYTOPLASMIC (S1 OF REPEAT
                                                                                                                                                                                                                                     CYTOPLASMIC
S5 OF REPEAT
                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL) S4 OF REPEAT I.
                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL
                                                                                                                                                                                                                                   REPEAT I.
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CA_BIND
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DOMAIN
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                                                                                                                                                                                                                                                                                               32 LWGGDPVVPWSCRFCSQQDDGQD----RERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                                                                                                                                                                                                                                                                        Local Similarity
                         TCLTGSSPLSCWR-PEMVGLL--SLWDMTRM----LNMLIVFRFLRIIPSMKPMAVVAS
                                                                                                                                                                                      LFRRRLGTRAAFEVLSSMYGEGGAFPQATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSP
                                                                                                                                                                                                                                         YSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQF-----RGYLMKSLQTS
                                                                                                                                                                                                                                                                    LEGFDPPHPCGVQGCPAGYECKDWIGPNDGITQFDNILFAVLTVFQCITMEGWTTVL---
--LYFHSSFNCFDFGVTVGSIFEVVWAIFRPGTSFGISVLRALRLLRIFKITKYWASLRN
                                                    QVFYWIVLSLVALNTACVAIVHHNQPQWLTHLLYYAEFLFLGLFLLEMSLKMYGMGPR---
                                                                               ----WGFSTASSLCTTCWSCCSRSLP-WACE--
                                                                                                                                  WQTWCPFACSWCWMQMCCLLSVMTSS-----
                                                                                                                                                             IERELNGYRAWIDKAEEVM-----LAEENKNSGTSALEVLRRATIKRSRTEAMTRDSSD-
                                                                                                                                                                                                                 YNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRAFMKLRRQQQ
                                                                                                                                                                                                                                                                                                                          102;
                                                                                                        ·------EHCVDISSVGTPLARASIKSAKVDGASYFRHKERLLRISVRHAVKS
                                                                                                                                                                                                                                                                                                                                                                              2259 AA;
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18.1%;
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BY SIMILARITY.

PHOSPHORYLATION (BY CAPK) (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

HERRQLEPVPPKPRPLLSYSSLKQQPSNFSPPADGSQGGSL
LASPALESAQVGLPESSDSPRRAQGSHASPQRYISEPYLAL

HEDSHASDGGEETLTPEAAVATSLGRANTIGSAPPLHSW
QMPNGHYRRRRGGPGAGALCGAVGDLLSDTEEDKC -> Q
QWGPQEEGVLLHPHQGCGWPCRDRRWAPGRRGWSGEKSHSP
                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT III.
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV.
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT IV.
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT IV.
                                                                                                                                                                                                                                                                                                                                                                              MW;
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POLY-GLU.
POLY-ARG.
POLY-ARG.
POLY-VAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-SER.
POLY-ARG.
BINDING T
                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                   Score 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL) S4 OF REPEAT IV. CYTOPLASMIC (POTENTIAL). S5 OF REPEAT IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
CALCIUM ION SELECTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALCIUM ION SELECTIVITY AND PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALCIUM ION SELECTIVITY AND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
CALCIUM ION SELECTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                         LPHCGRDSTGGAGQGPPRYCGSGAGDAGGTCDSLSP
                                                                                                                                                                                                                                                                                                                                                                                              ISOFORM BII-2
                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                        No.
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                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                          207;
                                                                                                                                                                                                                                                                                                                          Indels 162;
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STANDARD;

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01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Voltage-dependent L-type calcium channel alpha-1s subunit channel, L type, alpha-1 polypeptide, isoform 3, skeletal CACNAIS OR CACNAIS OR CACNAIS OR CACNIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Lagomorpha; Leporid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88336904; PubMed-2458626;
Ellis S.B., Williams M.E., Ways N.R., Brenner R.,
Leung A.T., Campbell K.P., McKenna E., Koch W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanabe T., Takeshima H., Mikami A.,
Kangawa K., Kojima M., Matsuo H., H
                                                                                                                        DIHYDROPYRIDINE-BINDING SITE.
MEDLINE-92021019; PubMed-1656465;
                                                                                                                                                                                                                                                   "Identification of a phenylakylamine binding region subunit of skeletal muscle Ca2+ channels.";
                                                                                                                                                                                                                                                                                                                    Striessnig J., Glossmann H., Catterall W.A.;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91067656; PubMed=2174553;
                                                                                                                                                                                                                                                                                                                                                                                  PHENYLALKYLAMINE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Calcium channel beta-subunit binds to a conserved motif in cytoplasmic linker of the alpha 1-subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA-SUBUNIT BINDING DOMAIN. MEDLINE=94150724; PubMed=75(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence and expression of subunits of a DHP-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Primary structure of the skeletal muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87258269; PubMed=3037387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7509046;
1,4-dihydropyridine binding regions within skeletal muscle Ca2+ channels by photoaffir
                                                                                          Striessnig
                                                                                                                                                                                                                      U.S.A.
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                                                                                       J.,
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                                                                                          Glossmann H., Catterall W.A.,
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S.;
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Hui A., Sch
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   PARGE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RT PACTICALLY, CALCULANT, CALCULANT, WAR, FACTOR OF DEFINITION OF CALCIUM CHANNELS (VSCC) MEDIATE THE CC IN A VARIETY OF CALCIUM CINS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CCELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S COUPERACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S COUPLED BELOCKED BY DIHYDROPYRIDINES (DHP), CALCIUM CHANNELS BELOCKED BY DIHYDROPYRIDINES (DHP), PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-GARTOXIN-IIIA (OMEGA-GAR-IIIA). THEY ARE HOMEVER INSENSITIVE TO OMEGA-CONOTOXIN-C GVIA (OMEGA-CTA-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-CONOTOXIN-C GVIA (OMEGA-CON-CONTRACTION COMPLING IN SKELETAL MUSCLE. COUTLING IN EXCITATION-CONTRACTION CHANNELS ARE MULTISUBUNIT CONFLICTS, CONSISTING OF ALPHA-1S SUBUNIT PLAY AN IMPORTANT COUPLIES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNIT SUBUNIT IS SUPFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CHANNEL ACTIVITY. THE BUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CHANNEL ACTIVITY. THE BUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CHANNEL ACTIVITY. THE BUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CHANNEL ACTIVITY. THE SUBUNIT IS DERECTED TO COUPLING THE CHANNEL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                        --- TISSUE SPECIFICITY: SKELETÄL MUSCLE SPECIFIC.
--- IDOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
--- IDOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
--- ITERNSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
--- PROBABLY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
--- PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
--- IDOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE
RYANODINE RECEPTOR, AND IS THERREPORE IMPORTANT FOR CALCIUM RELEASE
FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION.
--- PTM: THE ALPHA-1S SUBUNIT IS FOUND IN TWO ISOFORMS IN THE SKELETAL
MUSCLE: A MINOR FORM OF 121 KDA CONTAINING THE COMPLETE AMINO ACID
SEQUENCE, AND A MAJOR FORM OF 190 KDA DERIVED FROM THE FULL-LENGTH
FORM BY POST-TRANSLATIONAL PROTEOLYSIS CLOSE TO PHE-1690.
--- PTM: BOTH THE MINOR AND MAJOR FORMS ARE PHOSPHORYLATED IN VITRO BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Striessnig J., Murphy B.J., Catterall W.A.; "Dihydropyridine receptor of L-type Ca2+ channels: identification of binding domains for [3H](+)-PN200-110 and [3H]azidopine within the
                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roehrkasten A., Meyer H.E., Nastainczyk W., Sieber M., Hofmann F., "CAMP-dependent protein kinase rapidly phosphorylates serine-687 o the skeletal muscle receptor for calcium channel blockers."; J. Biol. Chem. 263:15325-15329(1988).
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                                                                                                                        ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                         FAMILY.
                                                                                                                                                                                                                                                                                                                    FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Ellis S.B., Leung A.T., Harpold M.M.

TISSUE=Skeletal muscle;

FROM N.A.

Nature

TISSUE-Skeletal muscle; SEQUENCE FROM N.A.,

AND

Science

Nature 368:67-70(1994).

Pragnell M., d Campbell K.P.;

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"Identification alpha 1 subunit Kanaoka Y. Nakayama

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BL; M23919; AAA31159.1; -.

R; A30063; A30063.

iterPro; IPR002077; Ca_channel.

iterPro; IPR00211; Cat_channel_TrpL.

iterPro; IPR00636; Cation_chan_non_lig.

iterPro; IPR001682; Channel_pore_Ca_Na.
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M. Channel; Glycoprotein; Repeat; Multigene M. Channel; Glycoprotein; Polymorphism.
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S3 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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S1 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT I (POTENTIAL).
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BINDING TO THE BETA SUBUNIT
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; Repeat; Multigene
                                (BY SIMILARITY).
CALCIUM ION SELECTIVITY
                                                                     CALCIUM
                                                                                                                                                            EXTRACELLULAR
                SIMILARITY)
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ION SELECTIVITY AND PERMEABILITY
                                                                     ION SELECTIVITY AND
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                                 AND PERMEABILITY
                                                                     PERMEABILITY
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RESULT 12
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Best Local
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            MEDLINE=96435439; PubMed=8838325; Hogan K., Gregg R.G., Powers P.A.; "The structure of the gene encoding the human skeletal muscle alpha subunit of the dihydropyridine-sensitive L-type calcium channel (CACNLIA3).";
                                                                                                                                                                                                                                                                                           CCAS_HUMAN STANDARD; PRT; 1873 AA. Q13698; Q13934; Q12896; 15-JUL-1999 (Rel. 38, Created) 16-JUL-1999 (Rel. 38, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Voltage-dependent L-type calcium channel alpha-1s channel, L type, alpha-1 polypeptide, isoform 3, s CACNA1S OR CACNLIA3 OR CACH1 OR CACNI.
                                                                                                                   dihydropyridine-sensitive L-type Genomics 24:608-609(1994).
                                                                                                                                          Hogan K., Powers P.A., Gregg R.G.; "Cloning of the human skeletal muscle
                                                                                                                                                                                          TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                    SEQUENCE
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                          MEDLINE=95229168; PubMed=7713519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNMLIVFRELRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITHFDNFGFSMLTVYQCITMEGWTDVL---YWVNDAIGNEWPWIYFVTLILLGSFFILNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KMSRGLPDKT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPLAGTPEATYQMTVELLFRDILEEPGEDELTERLSQHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCT----TCWSCCSRSLP-WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---WCWMQMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAYGGPSYPGVLVCIYFIILFVCGNYILLNVFLAIAVDNLAEAESLTSAQKAKAEERKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRYSGPWSK-----KWDPRSHL
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                                                                                      FROM N.A.
31:392-394(1996).
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Pred. No. 9
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                                                                                                                                  calcium
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channel (CACNL1A3).";
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ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, VORIENT OR EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUGOTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-GAGATOXIN-IIIA (OMEGA-AGA-IIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GALCIUM CHANNELS CONTANING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT ROLE IN EXCITABION-CONTRACTION COUPLING IN SKELETRAL MUSCLE. TO SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERACE VOLTAGE-SENSITYE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hogan K.,
Fontaine
"A calciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDITINE-97342905; pubmed-119552; Monnier N., Procaccio V., Stieglitz P., Lunardi J., Marchi Procaccio V., Stieglitz P., Lunardi J., Walignant-hyperthermia susceptibility is associated with a mutation of the alpha-1-subunit of the human dihydropyridine-sensitive L-type voltage-dependent calcium-channel receptor in skeletal muscle."; Am. J. Hum. Genet. 60:1316-1325(1997).

1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
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q32.
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Submitted (JUL-1995) to the EMBL/Campania.
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SEQUENCE
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"Dihydropyridine receptor mutations cause paralysis.";
Cell 77:863-868(1994).
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Kwiecinski H., McManis P.G., Santiago
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MEDLINE-94273190; PubMed-8004673;
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         SUBCELLULAR LOCATION: Integral membrane protein.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.

DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS ($1, $2, $3, $5, $6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT ($4). $4 SEGMENTS
POSITIVELY CHARGED AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED ANION ACIDS AT EVERY THIRD POSITION.

SERIES OF POSITIVELY CHARGED ANION ACIDS AT EVERY THIRD POSITION.

DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE
RYANDDINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calcium channel mutation causing hypokalemic periodic paralysis.", n. Mol. Genet. 3:1415-1419(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.G., Couch F., Hogan K., Powers P.A.; ment of the human gene for the alpha-1 subunit of the skeletal DHP-sensitive calcium channel (CACNLIA3) to chromosome 1q31-
    THE
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Lehmann-Horn F., Elbaz A., Heine J
P.A., Lapie P., Vale-Santos J.E.,
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- PTM: PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL
- FUNCTION (BY SIMILARITY).

 DISEASE: DEFECTS IN CACNAIS ARE THE CAUSE OF HYPOKALEMIC PERIODI PARALYSIS (HYPOKEP OR HOKEPI), AN AUTOSOMAL DOMINANT SKELETAL MUSCLE DISORDER MANIFESTED BY EFISIODIC WEAKLESS ASSOCIATED WITH HYPOKALEMIC PERIODIC TO ALTERED
- LOW SERUM POTASSIUM. MUSCLE WEAKNESS COULD BE DUE TO ALTEREE EXCITATION-CONTRACTION COUPLING IN HYPOKPP PATIENTS. DISEASE: DEFECTS IN CACNALS ARE THE CAUSE OF MALIGNANT HYPERTHERMIA SUSCEPTIBILITY 5 (MHS5); AN AUTOSOMAL DOMINANT DISORDER THAT IS POTENTIALLY LETHAL IN SUSCEPTIBLE INDIVIDUA EXPOSURE TO COMMONLY USED INHALATIONAL ANESTHETICS AND DEPOLARIZING MUSCLE RELAXANTS.
 SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY. DOMINANT INDIVIDUALS AND õ

modified and entities requ European SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r requires non-profit equires a license agreement (email to license@isb-sib.ch) this statement institutions as long as its content is not removed. Usage by and removed. Usage by and removed. Isage by and removed. Agreement (See http://www.isb-sib.ch/announce/ and no through the restrictions EMBL ŝ a collaboration outstation -5 in no way

J30707; AAB37235.1
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Ionic channel; Transmembrane; Ion transport; Volt Calcium channel; Glycoprotein; Repeat; Multigene Calcium-binding; Phosphorylation; Disease mutatio
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MAN STANDARD; PRT; 2221 AA. Q99025; Q99241; Q13917; Q13922; Q13919; Q13925; Q13926; Q13927; Q13928; Q13930;
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MEDIINE=97242615; PubMed=9087614; Kloeckner U., Mikala G., Eisfeld J., Iles Kloeckner U., Mikala G., Eisfeld J., Iles Mershon J.L., Schwartz A., Varadi G.; "Properties of three COOH-terminal splice L-type Ca2+-channel alphal-subunit."; Am. J. Physiol. 272:H1372-H1381(1997).
                                                                                                                                                                                                                                                                                 Melvin D., Varadi G., Schwartz A.;

"Cloning, chromosomal localization, and function

alphal subunit of the L-type voltage-dependent

normal human heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q13923; Q13933; Q13932; Q15877; Q99875; Q14744; Q14743; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Voltage-dependent L-type calcium channel alpha-1C subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle). CACNAIC OR CACNLIA1 OR CCHLIA1 OR CACH2 OR CACN2.
Submitted (MAR-1998) [9]
                                                                                                                                                                                                         TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                        Schultz D., Mikala G., Yatani A., Engle Sinke R.J., Weghuis D.O., Kloeckner U.,
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93317655; PubMed=8392192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soldatov N.M., Zuelke R.D., Bouron A., "Molecular structures involved in L-typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Hippocampus;
MEDLINE=97166207; PubMed=9013606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic structure of human L-type Ca2+ channel.";
Genomics 22:77-87(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung fibrol MEDLINE=95048396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
                                       Soldatov N.M.
                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional expression of splice channel (isoform 1 gene).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soldatov N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Different voltage-dependent inhibition Ca2+ channel splice variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soldatov N.M., Bouron A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fibroblast;
MEDLINE=95256214; PubMed=7737988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soldatov N.M.;
                                                       SEQUENCE FROM N.A. (ISOFORMS ALC-105 AND ALC-106)
                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inactivation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (HFCC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92262493; PubMed=1316612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroblasts."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
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                                                                                                                                                                                                                                                                Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blast, and Hippocampus;
PubMed=7959794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORMS HHT-1;
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                   EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                            HT-1
                                                                                                                                                                                                                                                                90:6228-6232(1993).
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Catarrhini;
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Wakamori M.,
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J. BIOL. Chem. 268:13026(1993).

J. BIOL. Chem. 268:13026(1993).

11- FUNCTION: VOLTAGE-SENSITYE CALCIUM CHANNELS (VSCC) MEDIATE THE FUNCTION: VOLTAGE-SENSITYE CALCIUM CHANNELS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1C GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIMYDROPRILDINES (DHP), PHENYLALKYLAMINES, BENZOTHLAZEPINES, AND BY OMEGA-AGATOXIN-IIIA (OMEGA-CTX-GVIA) AND DMEGA-AGTOXIN-IVA (OMEGA-AGA-IIIA). THEY ARE HOMEVER INSENSITIVE TO OMEGA-AGA-IVA).

CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT ROLE IN EXCITATION-CONTANTACTION COUPLING IN THE HEART.

-1- SUBUNIT: VOLTAGE-SENSITIVE ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNIT SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SUBCELLULAR LOCATION: INTEGRAL ACTIVITS BETA AND ALPHA-2/DELTA ALL THESE SPLICE VARIANTS PROBABLY COMPOSE CHANNELS WITH DIFFERENT GATING PROPERTIES, AND DISPLAY MARKED DIFFERENCES IN THE SENSITIVETY OF ONE OF CAMPOINTS WARKED DIFFERENCES IN THE SENSITIVETY OF ONE OF CAMPOINTS WARKED DIFFERENCES IN THE SENSITIVETY OF ONE OF CAMPOINTS WARKED DIFFERENCES IN THE SENSITIVETY OF ONE OF CAMPOINTS WARKED DIFFERENCES IN THE SENSITIVETY OF ONE OF CAMPOINTS WARKED DIFFERENCES IN THE SENSITIVETY OF ONE OF CAMPOINTS WARKED DIFFERENCES IN THE SENSITIVE TO THE CAMPOINT OF THE PROPERTIES.
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Powers P.A., Gregg R.G., Lalley P.A., Liao M., Hogan K.;
Passignment of the human gene for the alpha 1 subunit of the cardiac
DHP-sensitive Ca2+ channel (CCHLIA1) to chromosome 12p12-pter.";
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"Molecular diversity of L-type calcium channels. Evidence for alternative splicing of the transcripts of three non-allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mapping of a human brain voltage-gated calcium channel to human chromosome 12p13-pter.";
                                                                                                                                                            SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTINHIBITS THE OPENING OF THE CHANNEL (BY SIMILARITY).
                                                                                                                                                                                                                                                 DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Localization of ion selectivity sites within the pore of them. 268:13026-13029(1993).

UNCTION: VOLTAGE-SENSTERM:

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                                                                                  BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
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b; Pred. No. 1.7e
74; Mismatches
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1.7e-06;
159;
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Genomics 14:1092-1094(1992).

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TISSUE SPECIFICITY: EXPRESSED CELLS AND IN THE BRAIN.

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J.D.,

MEDLINE=93122776; PubMed=1335957;

SEQUENCE OF 1196-1421 FROM N.A.

Genomics

10:835-839(1991).

TISSUE-Brain;

SEQUENCE OF 1140-1206 FROM N.A.

Chem. 265:20430-20436(1990).

MEDLINE-91056091;

PubMed=2173707;

TISSUE-Heart

SEQUENCE OF 1182-1503 FROM N.A. (ISOFORMS CACH2A; CACH2C AND CACH2D).

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RA FUILEA Y., WADILEEF M., DIRKSER R.T., Kim M.-S., Niidome T., Nakai J.,
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RA MIKOSHIDA K., MOTI Y., Beam K.G.;
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CCAB_RABIT
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Oryctolagus cuniculus (Rabbit).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Leporidae; Oryctolagus.
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Q05152;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Voltage-dependent N-type calcium channel alpha-1B subunit (Calcium channel, L type, alpha-1 polypeptide isoform 5) (Brain calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93236885; PubMed=8386525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002077; Ca_channel. TrpL. InterPro; IPR002111; Cat_channel.TrpL. InterPro; IPR000536; Cation_chan_non_lig. InterPro; IPR001682; Channel_pore_Ca_Na. Pf4mg, Pf00520; ion_trans; 4.
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CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT IV (POTENTIAL)
                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT III (POTENTIAL).
                                                                                 S2 OF REPEAT IV (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT IV (POTENTIAL).
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$3 OF REPEAT III (POTENTIAL).
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S2 OF REPEAT IV (POTENTIA
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S1 OF REPEAT IV (POTENTIAL).
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S4 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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S1 OF REPEAT II (POTENTIAL)
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S6 OF REPEAT I (POTENTIAL).
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S5 OF REPEAT I (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL).
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S1 OF REPEAT
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                                                                                                                                                                                                   NGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLDAYRRYS-----GPWS
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CYTOPLASMIC (POTENTIAL).
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Pred. No.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
M; 0413DA93794C8B34 CRC64;
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PHOSPHORYLATION (BY CAPK) (POTENTIAL)
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(BY SIMILARITY).
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
voltage-dependent L-type calcium channel alpha-1C subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle)
(Smooth muscle calcium channel blocker receptor) (CACB-receptor).
CACNAIC OR CACNIIAL OR CCHLIAL OR CACHZ OR CACNZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89330539; PubMed-2474130; Mikami A., Imoto K., Tanabe T., N. Narumiya S., Numa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "primary structure and functional expression of a high voltage activated calcium channel from rabbit lung.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sensitive L-type calcium channels.";
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Heart, and MEDLINE-90382589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dihydropyridine-sensitive calcium channel.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "primary structure and functional expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                              MEDITINE 92387386; PubMed = 1325377; Yoshida A., Takahashi M., Nishimura S., Ta "Cyclic AMP-dependent phosphorylation and dihydropyridine-sensitive Ca channel."; FEBS Lett. 309:343-349(1992).
                                                                                                                                                                                                                                           Ren D., Xu H., Eberl D.F., Chopra M., Hall L.M.;
"A mutation affecting dihydropyridine-sensitive current levels and activation kinetics in Drosophila muscle and mammalian heart calciuchannels.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 340:230-233(1989).
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94050141; PubMed=8232554; Yang J., Ellinor P.T., Sather W.A., Zhang J.-F., Ts: "Molecular determinants of Ca2+ selectivity and ion L-type Ca2+ channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      perez-Reyes E., Wei X., Castellano A., Birnbaumer L., "Molecular diversity of L-type calcium channels. Evic alternative splicing of the transcripts of three non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Tissue specific expression of high voltage activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hofmann F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett.
"Calcium channel beta-subunit binds to a conserved motif in the I-II cytoplasmic linker of the alpha 1-subunit.";
                                                               BETA-SUBUNIT BINDING DOMAIN.
MEDLINE=94150724; PubMed=7509046;
                                                                                                                                                                                                                                                                                                                                                             Nature 366:158-161(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1192-1485 FROM N.A. (ISOFORM CACH2C)
                                Pragnell M., de Waard M., Mori Y., Campbell K.P.;
                                                                                                                                                                                                PHOSPHORYLATION BY CAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGENESIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDLINE=91056091;
                                                                                                                                                                                                                                                                                                                                MUTAGENESIS OF CYS-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hullin R., Freundner S., Singer D., Dascal N., Flockerzi V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem. 265:20430-20436(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269:409-412(1990).
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                                                                                                                                                                                                                                18:2335-2341(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2173707;
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                                                      Tanabe T., Snutch T.P.,
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                                                                                                                                                    Takeshima H., nd regulation (
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of the ca
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EMBL; X15539; CAA33546.1; -.
EMBL; X55763; CAA39289.1; -.
EMBL; M57974; AAA31182.1; -.
EMBL; X60782; CAA43196.1; -.
PTR; S05054; S05054.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN A VARIETY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL DOTTISION AND CELL DEATH. THE ISOFORM ALPHA-1C GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DIP), PHENYLALKYLAMINES, BENZOTHARAEPINES, AND BY OMEGA-AGA-CONOTOXIN-GOVIA (OMEGA-CTX-GVIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGACOXIN-IVA (OMEGA-CTX-GVIA). CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-1C SUBUNIT SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE POREFORMING AND VOLTAGE-SENSITIVE ALPHA-2, BETA AND DELTA SUBUNITS IN ALTERNATIVE TO GENERATE VOLTAGE-SENSITIVE ALCIUM CHANNEL ACTIVITY. THE AUXILLARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

-1- SUBCLELULAR LOCATION: INTEGRAL MEMBERS PROBLED BY ALTERNATIVE SPLICING.

-1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; THE HEART ISOFORMS CACHZA (SHOWN HERE), CACHZC, CACHZD AND A LUNG ISOFORM; ARE PROBLED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: EXPRESSION IN CARDIAC MUSCLE IN LUNG, EXPRESSED IN ALFWAY AND VASCULAR SMOOTH MUSCLE CELLS.

-1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHORIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE PROBLEM REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

-1- DOMAIN: BINDING OF INTRACELLULAR CACCIUM THROUGH THE EF-HAND MOTIF INHIBITS THE OPENING OF THE CALCIUM THROUGH THE EF-HAND MOTIF INHIBITS.
                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                     Calcium channel; Glycoprotein; Rep
Calcium-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by ar
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                                               REPEAT
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Science 270:1502-1505(1995)
-!- FUNCTION: VOLTAGE-SENST
                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de Leon M., Wang Y., Jones L., Perez-Reyes E., Wei X., Soong T.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EF-HAND MOTIF AND CALCIUM INACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:67-70(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96095215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: VOLTAGE SENSÍTIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
                                                                                                                                                   channel;
                                               141
540
917
                                                                                               Transmembrane; Ion transport; Voltage-gated channel; l; Glycoprotein; Repeat; Multigene family; g; Phosphorylation; Alternative splicing.
                                                                                                                                                                    ion_trans; 4.7; CACHANNEL.
    438
786
1199
1509
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CYTOPLASMIC (POTENTIAL)
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Db	Qу	Дb	VΩ	В	Qy	Db	Qy	Д и м а	H H	FT	FT	FT.	FT.	n Fi	E E	H) H	1 H 1	7 F)	H H	FT	T T	F F	F	F F T	FT	FI	F 7	EJ.	F F	E F	1 H	된 된	FT	o Fi	FT	11 H	H H	FT	FT FT
532 FSRYW 204 CWMQM	157 FPQAT	478 DPENE	126	: 418 LVIFG	101 FTVIG	362 CKPGWDG-	46 CSQQI	Query Match Best Local Simi Matches 99;	DOMAIN	DOMAIN	TRANSMEM	TRANSMEM DOMAIN	DOMAIN	DOMAIN	DOMAIN TRANSMEM	TRANSMEM	TRANSMEM	TRANSMEM	TRANSMEM DOMAIN	DOMAIN	DOMAIN	TRANSMEM	TRANSMEM	TRANSMEM DOMATN	DOMAIN	DOMAIN	TRANSMEM	TRANSMEM	TRANSMEM	TRANSMEM DOMAIN	DOMAIN	DOMAIN TRANSMEM	TRANSMEM	TRANSMEM	DOMAIN	DOMAIN	TRANSMEM	TRANSMEM	TRANSMEM DOMAIN
FSRYWRRWNRFCRR	PQATRRGPSTSLRFCRAP	DEGMDEE	1	SFFVLNL	SLFLMNL	DG-PKHG	DGQDRER	larit Conse	684	458	1482	1393 1413	1374	1331	1304 1312	1284	1250	1172	1062 1082	1043	1017	866 986	966	931 950	784	704	665 84	646	617	609	574	555 555	411	301	282	243 263	212	191	155 174
KCRAAVK	LRFCRAPSSSA	: KPRNMSMPTSI	MKSLQTS	:: : :: : SFFVLNLVLGVLSGEFSI	FTVIGSLFLMNLLTAIIYSQF-	THEDNEAFA	LTYFONLPES	6.8%; 18.6%; tive	690	475	1506	1412 1481	1392	1354	1311 1330	1303	1268	1196	1081 1171	1042	1023	997 1016	985	949	930	758	683 703	664 664	635 635	608 616	588	554 573	435	320	300	262 1	223 242	211	173 190
SRYWRRWNRFCRRKCRAAVKSNVFYWLVIFLVFLNTLTIASEHYNQPHWLTEVQDTAN- 590 WMQMCCLLSVMTSSWGFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTG 256	SATTTLTTWGTSSP-WQTWCPFACSW 203	S K 53	RAAFEVLSSMVGEGGA 1	 YLDWITQAEDI 47	RGYL 125	PKHGITNFDNFAFAMLTVFQCITMEGWTDVLYWMQDAMGYELPWVYFVS 417	SQQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIV 100	Score 179.5; DB 1; Length 2171; Pred. No. 3.7e-06; 86; Mismatches 181; Indels 167; Gaps	SIMILARITY). POLY-LEU.	SINDING TO THE BETA SUBUNIT (BY	H	⋗ӈ	S4 OF REPEAT IV. CYTOPLASMIC (POTENTIAL).	י בי	TOPLASMIC (EXTRACELLULAR (POTENTIAL). S2 OF REPEAT IV.	Η τ		S5 OF REPEAT III.	TOPLASMIC (XTRA	CYTOPLASMIC (POTENTIAL). S3 OF REPEAT III.	2 OF	1 OF	SO OF REPEAT II. CYTOPLASMIC (POTENTIAL).	XTRA	CYTOPLASMIC (POTENTIAL).	EXTRACELLULAR (POTENTIAL). S4 OF REPEAT II.	Η,	S2 OF REPEAT II.	XTRA	YTOPLASMIC	S6 OF REPEAT I.	Н.	<u>~</u> ۲	TRACELLULAR	CYTOPLASMIC (POTENTIAL). S3 OF REPEAT I.	OF REPEAT I	S1 OF REPEAT I. EXTRACELLULAR (POTENTIAL)

19;

Search	Db	Qy	Db	Qу	Вb	Qy	Ъ	Qy	Db
ch co	784	428	724	374	683	317	641	257	591
search completed: October 8, 2002, 10:03:30	784 DNLADAESLTSAQKEEEEEKERKKLARTASPEKKQEVVGKPALEEAKEEKI 834	428 ENFLKWDPRSHLQPLAGTPEATYQMTVELLFRDILEEPGEDEL 471	GMLV	374 AALVTLWNLMYVNNW-QVFLDAYRRYSGFWSKIYFVLWWLVSSVIWVNLFLALIL 427	683 SILLLLELFITIFSLLGMQLFGGKFNEDEMQTRRSTFDNFP 723		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	257 SSPLSCWRPEMVGLLSLWDMTRMLNWLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFG 316	KALLALFTAEMLLKMYSLGLQAYFVSLFNRFDCFIVCGGILETILVETKV 640

Search completed: October 8, 2002, 10:03:30 Job time: 31 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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342
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_inverteb:
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
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2634
1 MSSACWEATGRCRI
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Gapop 10.0 ,
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  MSSACWEATGRCRLGGGWMV.....PGEDELTERLSQHPHLWLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version
Copyright (c) 1993 - 2002
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sp_bacteria:*
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sp_phage:*
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sp_rvirus:*
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Q9UHB1
Q9UYZ6
Q9NYZ5
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                                                                                                                                        Q9ZT83
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                                       Q9nt82 homo sapien
Q9wtn5 rattus norv
Q9zt83 arabidopsis
Q94ki8 arabidopsis
Q9ulq1 homo sapien
Q9eqj0 mus musculu
Q948t1 arabidopsis
Q91wx9 rattus norv
Q923k6 rattus norv
Q923k6 rattus norv
Q923k6 mesocricetu
Q96057 halocynthia
Q95226 homo sapien
Q9nyz6 h
Q9nyz5 h
Q9jis7
                               Q9uhb1
                                                                                                                                                                                 Description
            homo
                                 homo
                      homo
         sapien
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162	162	162.5	162.5	163	163.5		164	164.5	165	167	167	167	167.5	167.5	167.5	168	168.5	169.5	169.5	170	170	171	171	172	174.5	175.5	177.5	179.5
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528	414	2321	2146	2365	1956	1740	2506	588	1518	1837	1765	1715	1981	1791	1791	751	2333	2373	1536	2435	1351	2295	2288	2169	1688	1834	2331	1981
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Q96P56	Q96P54	Q9PUM4	Q9PUM3	Q9JKU5	Q9Y5Y9	Q17314	Q9NS88	Q91ZP5	Q963L6	Q967R4	Q9R053	Q18840	Q9NZC8	Q9UI33	Q9UHE0	Q90Z28	089089	Q96RZ9	Q9NYY4	Q9W433	Q02789	Q9WUT2	980M60	Q9Z305	057483	Q9EQ59	Q9TTA4	Q923Z7
Q96p56 homo sapien	OMO	gallus	gall	mus mus	homo	cyane	Q9ns88 homo sapien	Q91zp5 mus musculu	schis	Q967r4 caenorhabdi	ω	caen	homo	OMO	5	Q90z28 sternopygus	ratt	homo		drosc	Q02789 mus musculu	Q9wut2 mus musculu	Q9wub8 rattus norv	Q9z305 cavia porce		Q9eq59 rattus norv	0	Q923z7 rattus norv

ALIGNMENTS

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RESULT 1
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Best Local S
Matches 222
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Q9NT82;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 42.5 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; All 37479; CAB70760.1; -. InterPro; IPR000636; Cation_chan_non_lig. InterPro; IPR001636; Cat_channel_TrpL. InterPro; IPR001631; Cat_channel_TrpL. InterPro; IPR001531; Cat_channel_TrpL. InterPro; IPR001531; Cat_channel_TrpL. InterPro; IPR001531; Cat_channel_TrpL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKFZP434M0223
                                                                                323
                                                                                                                                                                                                                                              263
                                                                                                                                                         WRPEMVGLLSLWDMTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVV 322
    YYVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNL
                                          YYVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNL
                                                                                                                                                                                                                                                                                                                          ll Similarity 99.6
222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA; 42546 MW;
                                                                                                                                                                                                                                                                                                                                                            44.8%;
99.6%;
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                            Score 1180; DB 4;
Pred. No. 6.4e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F01113FFFD4E35B2 CRC64;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 371;
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RESULT
Q9WTN5
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Best Local
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InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001220; Lectin_legB.
Pfam; PF00520; ion_trans; 2.
PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
SEQUENCE 819 AA; 94609 MW; A9D3ABAC37BF39E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 voltage-gated sodium and calcium channels."; Biochem. Biophys. Res. Commun. 270:370-376(2000). EMBL; AB018253; BAA77556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20218667; PubMed=10753632; Ishibashi K., Suzuki M., Imai M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TIEMBLIEL 12,
01-NOV-1999 (TIEMBLIEL 12,
01-DEC-2001 (TIEMBLIEL 19,
01-DEC-ATED CA CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of a novel form (two-repeat) protein
    662
                                                  398
                                                                                                                                                                                                                                                                                  487
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                                                                                                                                                                                                                                                                                                                                256
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    QTSHWSRLYFMTFYIVTMVV-MTIIVAFILEAFVFR
                                                                                                                   GNSSLAPANGS-APCGSFEQL----EYWANNFDDFAAALVTLWNLMVVNNWQVFLDAYRR
                                             YSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHK 433
                                                                                           ARWGLTPIDSSITRLGNKTKFGRKGYYYLNNFDNILNSFYTLFELTVVNNWYIIMEGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQLLRLFKLKKRYRNVLDTMFELLPRMASLGLTLLTFYYSFAIVGMEFFSGRLSPNCSTP
                                                                                                                                                                                                                                --FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVI---VALP
                                                                                                                                                                                                                                                                                                                                                                                                                         LLSVMTSSWGFSTASSLCTT---CW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLRFCRAPSSSSATTTLTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFNDIEKHKFKSLLLHKRTAIQHAYHLLVSQRRPAGISYRQFEGLMRFYKPRMSARE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAF-------PQATRRGPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFNTLENSIVNLFVLLTTANFPDVMMPSYSRNPWSCVFFIVYLSIELYFIMNLLLAVVFD
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                                                                                                                                                                                                                                                                                YGVELFMKVAGLGPVEYLSSGWNLFDFSLTAFAFLGLLAL-----TLNMEPFYFIVVLRP
                                                                                                                                                                                                                                                                                                                                                                           -INILVNSKAFQYFMYLVVAVNGVWILVETFMLKGGNFISKHVPWSY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RFLTFKALNQSNTPLLSLKDFYDIYEVAALQWKAKKNRQHWFDELPRTAFLIFKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           -GSSPL----SCWRP-----EMVGLLSLWDMTRMLNM-----LIVFR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.1%; 25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 345; DB 11;
Pred. No. 4.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       ----SCCSRSLPWACEGTCPTPATCLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGTSSPWQTW---CPFACSWCWMQMCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 819;
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                                                                                                                                                                                                                                                                                                                                                                         486
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                                                                                                                                                                                                                             RESULT 3

Q9Z79

ID Q9Z79

AC Q9Z79

AC Q9Z79

AC Q9Z79

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AC Q9Z79

CO C C Q9Z79

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149 292

QQGLTVFTSYGATLYQMFILFTTSNNPDVWIPAYKSSRWSSVFFVLYVLIGVYFVTNLIL

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Matches
                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                               -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BI
EMBL; AF071527; AAD11598.1; -.
EMBL; AC005142; AAD15312.1; -.
EMBL; AL161497; CAB77841.1; -.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR00182; Channel_TrpL.
InterPro; IPR00182; Channel_pore_Ca_Na.
InterPro; IPR003015; HLH_Myc.
InterPro; IPR00315; HLH_Myc.
InterPro; IPR001696; Na_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9ZT83;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE CALCIUM CHANDEL 19, Last annotation update)
PUTATIVE CALCIUM CHANDEL 19, Last annotation update)
F9H3.19 OR T5L23.5 OR NEL4G03560.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maggoliophyta; eudicotyledons; core eudicots; Rosidae;
Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                 SEQUENCE
                                                                                                                                               PROSITE; PS00038
                                                                                                                                                                                        PRINTS; PR00170; NACI SMART; SM00054; EFh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil
Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.
Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia
Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. COLUMBIA;
Huang E.N., Parnell L.D., de la Bastide M.
Dedhia N.N., McCombie W.R.;
"Genomic sequence of Arabidopsis Thaliana
                                                                                                                                                                                                                             Pfam; PF00036; efhand; 2. Pfam; PF00520; ion_trans; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                55
RERLTYFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g J., Ma P., Parnell L.D., Chen C.-N., T5L23 from chromosome IV, position 19
                                                    al Similarity
115; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U., Ma P., Parnell L.D., e K., Mayer K.F.X.; tted (MAR-2000) to the EM
                                                                                                                                                                    PS00038; HELIX_LOOP_HELIX; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLUMBIA;
                                                                                                                               724 AA;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                          NACHANNEL.
                                                                                                                               83856 MW;
                                                                    13.0%;
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                                                    84;
                                        Pred. No. /e .
4; Mismatches
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                                                                                       Score
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                                                                                                                               EBA3A27EB15BFE32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen C.N., Chen E.Y., Mewes
                                                                    342;
No.
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                                                                  7e-21;
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X
                                                                                       DB 10;
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                                                    144;
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                                                                                                                             CRC64;
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                                                                                       Length
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                                                                                           724;
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W.,
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RESULT 4
Q94KIB
ID Q94K
AC Q94K
DT 01-D
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DT 01-D
DT 01-D
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fischer M., Knight H., Amtmann A., Sanders D.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF360372; AAK39554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE CALCIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q94KI8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q94KI8
                                                                                                                                                                                          362 KISKEEFGLIFDELDDTRDFKINKDEFADLCQAIALRFQKEEVPSLFEHFPQIYHSALSQ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 FNLLVMGNWQVWMESYKDLTGTWWSITYFVSFYVITILLLLNLVVAFVLEAFFTELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 WNLMVVNNWQVFLDAYRRYSGPWSKI-YFVLWWLVSSVIWVNLFLALILENFLHKWD 435
                                                                                                                                                                                                                                                                                                                                                                                  55 RERLTYFONLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                568 CIYCSIGVQVFGGLVNA--GNKKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFE----QLEYWANNFDDFAAALVTL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 CLLSVMT----SSW--GFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 QLRAFVRSPNFGYAISFILIINFIAVVVETTLDIEESSAQKPWQV-AEFVFGWIYVLEMA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 KISKEEFGLIFDELDDTRDFKINKDEFADLCQAIALRFQKEEVPSLFEHFPQIYHSALSQ 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
RPEMVGLLSLWDMTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY
                                                                                                                 QLRAFVRSPNFGYAISFILIINFIAVVVETTLDIEESSAQKPWQV-AEFVFGWIYVLEMA
                                            --LKIYTYGFENYWREGANRFDFLVT-----
                                                                          CLLSVMT----SSW--GFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCW 263
                                                                                                                                                     SLR-FCRAPSSSSA------TTTLTTWGTSS--PWQTWCPFACSWCW-MQMC
                                                                                                                                                                                                                                                                     AVVYDSFKEQLAKQVSGMDQMKRRMLEKAFGLIDSDKNGEIDKNQCIKLFEQLTNYRTLP
                                                                                                                                                                                                                                                                                                                                                QQGLTVFTSYGATLYQMFILFTTSNNPDVWIPAYKSSRWSSVFFVLYVLIGVYFVTNLIL 301
                                                                                                                                                                                                                                                                                                               AIIYSQFRGYLMKSLQ-TSLFRRRLGTRA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PDENTFFSNGEWIRYLLLARMLRLIRLLMNVQRYRAFIATFITLIPSLMPYLGTIFCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LKIYTYGFENYWREGANREDELVT------WVI--VIGETATEIT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLR-FCRAPSSSA-----TTTLTTWGTSS--PWQTWCPFACSWCW-MQMC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --MVGEGGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39554.1; -.
84873 MW; 1CA978D6B8BFF445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 342; DB 10; Length 733; 24.1%; Pred. No. 7.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                             84; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                        --WVI--VIGETATFIT-----
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                                                                                                                                                                                                                                  -----FPQATRRGPST
                                                                                                                                                                                                                                                                                                                                                                                                                             144; Indels 134;
                                                                                                                                                                                                                                                                                                               ----AFEVLSS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ULQ1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 6:329-336(1999).
EMBL; AB032995; BAA86483.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O., "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
KIAA1169 PROTEIN (FRAGMENT).
         498
                                                                        287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFE----QLEYWANNFDDFAAALVTL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YFONLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
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RPLOLLRLFKLKERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIVFPNCC
                                 R---FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALPG
                                                                                                                                                                                                                                                 FKGINILVKSKAFQYFMYLVVAVNGVWILVETFMLKGGNFFSKHVPWSY------LVFL
                                                                                                                                                                                                                                                                                                                   ----SVMTSSWGFSTASSLCTT---CW-----SCCSRSLPWACEGTCPTPATCL
                                                                                                                                                                                                                                                                                                                                                                              RERYLTFKALNQNNTPLLSLKDFYDIYEVAALKWKAKKNREHW-----FDELPRTALLI 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFNDIEKRKFKSLLLHKRTAIQHAYRLLISQRRPAG----ISYRQFEGLMRFYK-PRMSA 335
                                                                                                                             TIYGVELFLKVAGLGPVEYLSSGWNLFDFSVTVFAFLGLLAL----ALNMEPFYFIVVL
                                                                                                                                                                                     T------GSSPL----SCWRP-----EMVGLLSLWDMTRMLNM-----LIVF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFSTLENSIVSLFVLLTTANFPDVMMPSYSRNPWSCVFFIVYLSIELYFIMNLLLAVVFD 280
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IPR001682; Channel_pore_Ca_Na
IPR001220; Lectin_legB.
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Pred. No. 7.6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TWGTSSPWQTWCPFACSWCWMQMCCLL-
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9EQJ0
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL; AF217002; AAG44100.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C3H/HE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001220; Lectin_legB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 NSSLAP------ANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQVFLD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               614 GVTSQTSHWSRLYFMTFYIVTMVV-MTIIVAFILEAFVFR 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 LLSVMTSSWGFSTASSLCTT---CW-----SCCSRSLPWACEGTCPTPATCLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLTAIIYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTSTVADAYRWRNHTVGNRTV----VEEGYYYLNNFDNILNSFVTLFELTVVNNWYIIME 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVGEGGAF------PQATRRGPST 167
                                                                                                                                                                                                                                                   LQLLRLFKLKKRYRNVLDTMFELLPRMASLGLTLLTFYYSFAIVGMEFF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFSTLENSIVNLEVLLTTANFPDVMMPSYSRNPWSCVFFIVYLSIELYFIMNLLLAVVFD
inegvtsQtshwsrlyfmtfyivtmvv-mtiivafileafvfr 694
                                                             FLDAYRRYSGPWSKIYFVLWWLVSSVIWVNLFLALILENFLHK 433
                                                                                                                       RLTPNCCNTSTVADAYRFINHTVGNKTKVEEGYYYLNNFDNILNSEVTLFELTVVNNWYI
                                                                                                                                                                                  SLAP--ANGSAPCGSF------EQLEYWANNFDDFAAALVTLWNLMVVNNWQV 390
                                                                                                                                                                                                                                                                                                             --FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVYYVFAIIGINLFRGVIVALPGNS 345
                                                                                                                                                                                                                                                                                                                                                                              YGVELFMKVAGLGPVEYLSSGWNLFDFSVTAFAFLGLLAL----TLNMEPFYFIVVLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLRFCRAPSSSSATTTLTT-------WGTSSPWQTW---CPFACSWCWMQMCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFNDIEKHKFKSLLLHKRTAIQHAYGLLASQRRPAGISYRQFEGLMRFYKPRMSARE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -INILVNSKAFQYFMYLVVAVNGVWILVETFMLKGGNFTSKHVPWSY-----LVFLTI 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00520;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GSSPL----SCWRP-----EMVGLLSLWDMTRMLNM-----LIVFR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -RFLTFKALNQSNTPLLSLKDFYDIYEVAALQWKAKRNRQHWFDELPRTAFLIFKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00520; ion_trans; 2.
00520; ion_trans; 2.
PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%;
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19,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 342; DB 11; Length 817;
Pred. No. 8e-21;
70; Mismatches 156; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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RESULT Q91WX9

Q91WX9;

PRELIMINARY;

PRT;

1643 AA

SS DI DI ACI

Eukaryota;

01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

VOLTAGE-GATED CALCIUM CHANNEL PORE FORMING SUBUNIT CAV1.3ALPHA1. Rattus norvegicus (Rat).

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT 7
Q948T1
ID Q948
AC Q948
AC Q948
DT 01-I
DT 01-I
DT 01-I
OT 01-I
OT 01-I
OT 01-I
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Best Local
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21461266; PubMed=11577183; Furuichi T., Cunningham K.W., Muto S.; Furuichi T., Cunningham K.W., Muto S.; "A putative two pore channel AtTPC1 mediates Ca2+ flux in Arabidopsis "Beaf cells."; Plant Cell Physiol. 42:900-905(2001). Plant Cell Physiol. 42:900-905(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 KISKEEFGLIFDELDDTRDFKINKDEFADLCQAIALRFQKEEVPSLFEHFPQIYHSALSQ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302
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624
                                                                                                                                                                                                 324 YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFE----QLEYWANNFDDFAAALVTL 379
                                                                                                                                                                                                                                                                              518
                                                                                                                                                                                                                                                                                                                                               264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 -- MVGEGGA-----
                                                          380 WNLMYVNNWQYFLDAYRRYSGPWSKI-YFYLWWLVSSVIWVNLFLALILENFLHKWD 435
                                                                                                                                   577 CIYCSIGVQVFGGLVNA--GNKKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 RERLITYFQNLPESLISLLVLLITANNPDVMIPAYSKNRAYAIFFIVFTVIGSLFLMNLLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLLSVMT----SSW--GFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLRAFVRSPNFGYAISFILIINFIAVVVETTLDIEESSAQKPWQV-AEFVFGWIYVLEMA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLR-FCRAPSSSSA-----TTTLTTWGTSS--PWQTWCPFACSWCW-MQMC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVVYDSFKEQLAKQVSGMDQMKRRMLEKAFGLIDSDKNGEIDKNQCIKLFEQLTNYRTLF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQGLTVFTSYGATLFQMFILFTTSNNPDVWIPAYKSSRWSSVFFVLYVLIGVYFVTNLIL 301
                                                                                                                                                                                                                                                                                                                                        RPEMYGLLSLWDMTRMLNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIIYSQFRGYLMKSLQ-TSLFRRRLGTRA------AFEVLSS----
FNLLVMGNWQVWMESYKDLTGTWWSITYFVSFYVITILLLLLULVVAFVLEAFFTELD
                                                                                                                                                                                                                                                                          -PDENTFFSNGEWIRYLLLARMLRLIRLLMNVQRYRAFIATFITLIPSLMPYLGTIFCVL 576
                                                                                                                                                                                                                                                                                                                                                                                                                     --LKIYTYGFENYWREGANRFDFLVT------WVI--VIGETATFIT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.8%; Score 336; DB 10; 23.9%; Pred. No. 2.3e-20;
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                                                                                                                                          ----FETELAEDDYLLFTFNDYPNGMVTL
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RESULT 9
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                                                                                                                                                                                   0923K6 PRELIMINARY;
0923K6;
01-DBC-2001 (TrembLrel. 1
01-DEC-2001 (TrembLrel. 1
01-DEC-2001 (TrembLrel. 1
STRAIN-SPRAGUE-DAWLEY;
Mitchell J.W., Larsen J.K., Best P.M.;
"Identification of the Calcium Channel alphalE (Ca2.3)
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                         SEQUENCE FROM N.A
                                                                                          NCBI_TaxID-10116;
                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                    CALCIUM CHANNEL ISOFORM ALPHA1E7.
                                                                                                                                                                                                                                                                                                                                                           404 K-----IYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-SUPERIOR CERVICAL GANGLIA
                                                                                                                                                                                                                                                                                                                                      735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21380268; PubMed=11487617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 FLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 RRWRRWNRFNRRRCRAAVKSVTFYWLVIVLVFLNTLTISSEHYNQPDWLTQIQDIANKVL 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 SMPTSE--TESVNTENVSGEGETQGCCGSLWCWWKRRGAAKTGPSGCRRWGQAISKSKLS 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 TCWSCCSRSLPWACEGTCPTPA-----TCLTGSSP---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 RAPSSSSATTTLTIMGTSSPWQTWCPFACSWCWMQMCCLLSVMTSS---WGFSTASSLCT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 -----SKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKRNT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 KSLQTSLFRRRLGTRAAFEVLSS-------MVGEGGAFPQATRRGPSTSLRFC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 FQCITMEGWTDVL---YWVNDAIGWEWPWVYFVSLIILGSFFVLNLVLGVLSGEF----- 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 CR--SGWVGPNGGI------ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 LVLLTTANNPDVMIPAYSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 CRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQNLPESLTSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurosci.
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                                                                                                                                                                                                                                                                                                                                                                                        -------NFDETQTKRSTFDNFPQALLTVFQILTGEDWNAVMYDGIMAYGGPSS
                                                                                                                                                                                                                                                                                                                                                                                                                      SSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLRIFKVTRHWTSLSNLVASLLNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF-----
                                                                                                                                                                                                                                                                                                                               SGMIVCIYFIILFICGNYILLNVFLAIAVDN 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LALFTCEMLVKMYSLGLQAYFVSLFNRFDCFVVCGGITETILVELELMSPLGVSVFRCVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF370009; AAK72959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1643 AA; 186828 MW; 97AAA34B073EA520 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21:5944-5951(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%; Score 201; DB 11; Length 1643; 18.2%; Pred. No. 2.1e-08;
                                                                                                                                                                                   . 19, Created)
. 19, Last sequ
. 19, Last anno
                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 174; Indels 162;
                                                                                                                                                                                                                                                  2295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633
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RESULT 10
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DR
SQ
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                                                                                                        Q91W25
Q91W25;
           01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) VOLTAGE-GATED CALCIUM CHANNEL ALPHA1 SUBUNIT.
CAV1.3 (ALPHA1D).
                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed in Atrial Myocytes."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY029412; AAK33009.1; -.
                                                                                                                                                                                                                        652 QILTGEDWNEVLYNGIRSQGGVSSGMWSAIYFIVLTLFGNYTLLNVFLAIAVDN 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                381 NIMVVNNW-QVFLDAYRRY----SGPWSKIYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                                                                                                                                                                                                          324 ---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEYWANNFDDFAAALVTLW 380
                                                                                                                                                                                                                                                                                                                                                                                                                                  271 L--SLWDMTRM-----LNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 VHHNQPQWLTHLLYYAEFLFLGLFLLEMSLKMYGMGPR----LYFHSSFNCFDFGVTVGS 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 SSVGTPLARASIKSTKVDGASYFRHKERLLRISIRHMVKSQVFYWIVLSVVALNTACVAI 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 TTWGT----SSPWQTWCPFACSWCWMQMCCLLSV--MTSS----WGFSTASSLCTTCWSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 IERELNGYRAWIDKAEEVMLAEENKNSGTSALEVLRRATIKRSRTEAMTRDSSDEHCVDI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 LFRRRLGTRA----AFEVL--SSMVGEGGAFPQATRRGPSTSLR--FCRAPSSSSATTTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 YNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRAFMKLRRQQQ 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 LEGFDPPHPCGVQGCPAGYECKDWIGPNDGITQFDNILFAVLTVFQCITMEGWTTVL--- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 YSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQF-----RGYLMKSLQTS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 LWGGDPVVPWSCRFCSQQDDGQD----RERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                          IFEVVWAIFRPGTSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLF 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSRSLP-WACE-------GTCPTPATCLTGSSPLSCWR-PEMVGL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105;
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                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 191.5; DB 11; Length 2295; 22.2%; Pred. No. 2e-07; 10dels 103; Gaps
                                                                                                                           PRT;
                                                                                                                           1602 AA
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                                                                                     Matches
                                             Query Match
Best Local
                                                                                                                              TISSUE-HIT CELL;

MEDLINE-21329586; PubMed=11435619;

Scholze A., Plant T.D., Dolphin A.C., Nuernberg B.;

"Functional expression and characterization of a voltage-gated CaVI.3
(alphalD) calcium channel subunit from an insulin-secreting cell
                                                                                     SEQUENCE
                                                                                                                                                                                                                                                               Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata
                                                                                             Mol. Endocrinol. 15:1211-1221(2001).
EMBL; AJ311617; CAC48390.1; -.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Mesocricetus
                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                              NCBI_TaxID=10036;
6 WEATGR-CRLGG-----GWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLT 59
                               91;
                                             Similarity
                                                                                 1602 AA;
                                Conservative
                                          7.2%;
                                                                                                                                                                                                                                                      Rodentia;
                                                                               181297 MW; 420737B974DE2456 CRC64;
                               87;
                                         Score 190; DB 11;
Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Cricetinae;
                              Mismatches
                              173;
                                                     Length 1602;
                            Indels 158;
                                                                                                                                                                                                                                                   Cricetinae;
                          Gaps
                           18;
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                                                                    Matches
                                                                                                    Query Match
                                                                                                                                                                                                                     Okamura Y., Okagaki R.;
"TuCal, ascidian calcium channel alphal-subunit.";
submitted (MAY-1988) to the EMBL/GenBank/DDBJ data
EMBL; AB013604; BAA34927.2; -
InterPro: IPR000636; Catton_chan_non_lig.
InterPro: IPR002111; Cat_channel_TrpL.
InterPro; IPR002111; Cat_channel.
InterPro; IPR002177; Ca_channel.
InterPro; IPR001682; Channel.pore_Ca_Na.
                                                                                                                                                                                                                                                                                                                                                                                           Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID-7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation updat
aSCIDIAN CALCIUM CHANNEL ALPHA1-SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                096057;
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                                                                                                                                                      Pfam; PF00520; ion_trans; 4. PRINTS; PR00167; CACHANNEL. PRINTS; PR00170; NACHANNEL.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                             Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454
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                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 RIFKVTRHWTSLSNLVASILNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF-----
                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  717 MIVCIYFIILFICGNYILLNVFLAIAVDN 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 LAPANGSAPCGSFEQLEYWANNFDDFAAALVTLWNLMVVNNWQ-VFLDAYRRYSGPWSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 RIIPSMKPMAVVASTVLGLVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574 FVSLFNRFDCFVVCGGITETILVELELMSPLG-----------VSVFRCVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
   234
                              33 WGGDPVVPWSCRFCS-----QQDDGQDRERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFQNLPESLTSLLVLLTTANNPDVMIPAYSKNRAYA----IFFIVFTVIGSLFLMNLLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTFYWLVIVLVFLNTLTISSEHYNOPDWLTQIQDIANKVLLALFTCEMLVKMYSLGLQAY 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSWCWMQMCCL-LSVMTSS-----WGF---STASSLCTTCWSC-----CSRSLP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEEEGGEEGKR 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLSSMVG------EGGAFPQA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFDNFAFAMLTVFQCITMEGWTDVL---YWMNDAMGFELPWVYFVSLVIFGSFFVLNLVL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTSMPTSETESVNTENVSGEGETQGSCGSLCQAISKSKLSRRWRRWNRFNRRRCRAAVKS 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRRGPSTSLRFCRAPSSSSATTTLTTWGT-----SSPWQTWCPF-----A 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----IYFVLWWLVSSVIWVNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NFDETQTKRSTFDNFPQALLTVFQILTGEDWNAVMYDGIMAYGGPSSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------WACEGTCPTPATCLTGSSPLSCWRPEMVGLLSLWDMTRMLNMLIVFRFL 289
WG-----RHCSGGMICESDWAGPSKGIINFDTFYFAVITVFQCITMEGWTDVL--- 281
                                                                    99;
                                                                                     Similarity
                                                                                                                                                                                                          IPR001696; Na_channel.
                                                                                                                                        2125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                    Conservative
                                                                                     20.2%;
                                                                                                                                      242981 MW;
                                                                                  7.2%; Score 189.5; DB 5; Length 2125; 20.2%; Pred. No. 2.7e-07;
                                                                       76;
                                                                       Mismatches
                                                                                                                                         7C8B25B37A10F0C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                       159;
                                                                                                                                                                                                                                                                                                                databases
                                                                       Indels 157;
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346
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                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-UN-2001 (TIEMBLIEL 17, Last annotation update)
VOLTAGE-GATED L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Bech-Hansen N.T., Naylor M.J., Maybaum T.A., Pearce W.G., Koop B., Fishman G.A., Mcts M., Musarella M.A., Boycott K.M.; Fishman G.A., Mcts M., Boycott K.M.; Fishman G.A., Mccarle M.A., Paper in a novel retinal gene in xp11.23 cause incomplete CSMB."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF067227; AAD03587.1; -.

Interpro; IPR000636; Cation_chan_non_lig.

Interpro; IPR000636; Cation_chan_non_lig.

Interpro; IPR0006111; Cat_channel_TrpL.
                                                                                                                                                                                                                                                 InterPro; IPR002077; Ca_channel.
InterPro; IPR001682; Channel.pore_Ca_Na
Pfam; PF00520; ion_trans; 4.
PRINTS; PR00167; CACHANNEL.
SEQUENCE 1912 AA; 214031 MN; 0E2C450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACNA1F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 EFQKLREKQQTDEDMKGYMDWITQAEDLDPMNDEDREDRRSASNEQLNDADSEVSGLQID 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 AFEVL-----SSMVGEGGAFPQATRRGP-----STSLRFCRAPSSSSATTTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 YYMNDAVGNLWPWIYFVSLIIIGSFFVMNLILGVLSGEF-----SKEREKANARG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 GFSTASSLCTTCWSCCSRSLPWACEGTCPTPATCLTGSSPLSCWRPEM------ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 TTWGT-----SSPWQTW-----CPF---ACSWCWMQM----CCLLSVMTSSW 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 VNLFLALILEN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 IRSNEDTELQALLTVEQILTGEDWNVVMYNGIEAYGGASTIGLLTSVYFIVLEIGGNYIL 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 WANNFDDFAAALVTLWNLMVVNNWQVF----LDAYRRYS--GPWSKIYFVLWWLVSSVIW 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 LLNSIRSIASLLVLLFLFIIIFALLGMQMFGGRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 YSKNRAYA----IFFIVFTVIGSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRA 142
251 FFFAMLTVFQCVTMEGWTDVL---YWMQDAMGYELPWVYFVSLVIFGSFFVLNLVLGVLS
                                                                                                                                                                                  Local
                                       64 LPESLTSLLVLLTTANNPDVMIPAYSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIY 118
                                                                                                                       4 ACWEATGRCRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVQNMRAFGGILVVVY---YVFAIIGINLFRGVIVALPGNSSLAPANGSAPCGSFEQLEY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVSLFNREDCFVVCGGIVELVLTSSKIMEPLGISVLRCVRLLRIFKMTSSWNSLSNLVAS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETWWQMQRRALFKVCYSRRWRRWNRKTRRRCRTMVKSKSFYWLVIVLVFCNTLSLATEHY 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNVFLAIAVDN 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VGLLSLWD-----MTRM------LNMLIVFRFLRIIPSMKPMAVVASTVLG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RQPPWL-----TLAQDLANKILLTLFTIEMLVKMYSLGMQQY 488
                                                                                ACTLNQTECR -- GRWPGPNGGI-
                                                                                                                                                                   102;
                                                                                                                                                                                      Similarity
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                      7.2%; score 189; DB 4; Length 1912; 18.3%; Pred. No. 2.7e-07;
                                                                                                                                                                     79;
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                        0E2C45C8E4156E0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1912 AA
                                                                                                                                                                         Indels 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SEIEQEDK 590
                                                                                         -----TNFDN 250
                                                                                                                                                                           Gaps
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                                                                                                           Matches
                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                 InterPro; IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 4.
PRINTS; PR00167; CACHANNEL.
PRINTS; PR00170; NACHANNEL.
SEQUENCE 1977 AA; 220676 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
VOLTAGE-GATED L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Naylor M.J., Rancourt D.E., Bech-Hansen N.T.;
"Isolation and Characterization of a Calcium Channel Gene,
the Murine Orthologue of the Gene for Incomplete X-Linked of
Stationary Night Blindness.";
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR002077; Ca_channel.
InterPro; IPR001682; Channel_pore_Ca_Na.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 66:324-327(2000).
EMBL; AF201304; AAF15290.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=20334628; Pubmed=10873387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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     291
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                                                     4
  ACTINQTECR - - GRWPGPNGGI - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICGNYILLNVFLAIAVDN 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVSSVIWVNLFLALILEN 429
                                                ACWEATGRCRLGGGWMVPTGWVRGLELSLWGGDPVVPWSCRFCSQQDDGQDRERLTYFQN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDQTHTKRSTEDTEPQALLTVEQILTGEDWNVVMYDGIMAYGGPEEPGMLVCIYFIILE
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                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GILETTLVEVGAMQPLG------
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WMQ------MCCLLSV--MTSSWGFSTASSLCT----TCWSCCSRSLP
                                                                                             7.2%; Score 189; DB 4; L
18.3%; Pred. No. 2.8e-07;
7° Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RGYLMKSLQTSLFRRRLGTRAAFEVLSSMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                 354336550C6D8E73 CRC64;
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                                                                                                                                                      Length 1977;
                                                                                                      Indels
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RESULT 14
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                                                         Query Match
Best Local S
Matches 106
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01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                         Mittman S., Agnew W.S., Malek J.A.;
"Exon Organization and Alternative Splicing of CACNALE.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF223391; AAF37687.1; ---
EMBL; AF239258; AAF37687.1; JOINED.
EMBL; AF239259; AAF37687.1; JOINED.
InterPro; IPR000636; Catton_chan_non_lig.
InterPro; IPR002011; Cat_channel_TrpL.
InterPro; IPR002111; Cat_channel.
InterPro; IPR001682; Channel_Dore_Ca_Na.
Pfam; PF00520; ion_trans; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                     PRINTS; PR00167; CACHANNEL
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  LWGGDPVVPWSCRFCSQQDDGQD----RERLTYFQNLPESLTSLLVLLTTANNPDVMIPA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICGNYILLNVFLAIAVDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPESLTSLLVLLTTANNPDVMIPAYSKNRAYA----IFFIVFTVIGSLFLMNLLTAIIY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDQTHTKRSTFDTFPQALLTVFQILTGEDWNVVMYDGIMAYGGPFFPGMLVCIYFIILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSNLVASILNSMKSIASLLLLLFLFIIIFSLLGMQLFGGKF---
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                                                                                     Similarity
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                                                                                                                                                                  2224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TIEMBLIEL 15, Created)
(TIEMBLIEL 15, Last sequence update)
(TIEMBLIEL 17, Last anotation update)
NNEL ALPHALE SUBUNIT, DELTA39 SPLICE VARIANT
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                            7.2%;
19.4%;
                                                                                                                                                                     251889 MW;
                                                         91;
                                                                               Score 189;
Pred. No. 3.
                                                         Mismatches
                                                                                                                                                                  67D34234924F6690 CRC64;
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                                                      DB 4; I
1.2e-07;
nes 218;
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                                                                                                         Length 2224;
                                                         Indels 132;
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RESULT 15
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OT 01-OC
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"Exon Organization and Alternative Splicing of CACNAIE.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF23391; AAF37688.1; -.
EMBL; AF239258; AAF37688.1; JOINED.
EMBL; AF239258; AAF37688.1; JOINED.
InterPro; IPR000536; Cation_chan_non_lig.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR002077; Ca_channel.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CALCIUM CHANNEL ALPHAIE SUBUNIT, DELTA19 DELTA46 SPLICE VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                    InterPro; IPR001682; Channel_pore_Ca_Na
Pfam; PF00520; ion_trans; 4.
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                                                                                                                                                                                PRINTS; PR00167; CACHANNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 LEGFDPPHPCGVQGCPAGYECKDWIGPNDGITQFDNILFAVLTVFQCITMEGWTTVL--- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 TERLSQH 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 ANAQELTKDEQEEEEAFNQKHALQKAKEVSPMSAPNMPSIERDRRRRHHMSMWEPRSSHL 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 IMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWSAIYFIVLTLFGNYTLLNVFLAIAVDNL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 LFLLFIVVFALLGMQLFGGRFNFNDGTPSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 HCVDISSVGTPLARASIKSAKVDGVSYFRHKERLLRISIRHMVKSQVFYWIVLSLVALNT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 IERELNGYRAWIDKAEEVM-----LAEENKNAGTSALEVLRRATIKRSRTEAMTRDSSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 LFRRRLGTRAAFEVLSSMVGEGGAFPQATRRGPSTSLRFCRAPSSSSATTTLTTWGTSSP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   678 RERRRRH 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 LVTLWNLMVVNNW-QVFLDAYRRY----SGPWSKIYFVLWWLVSSVIWVNLFLALILENF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 EMVGLL--SLWDMTRM-----LNMLIVFRFLRIIPSMKPMAVVASTVLGLVQNMRAFGGI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACVAIVHHNQPQWLTHLLYYAEFLFLGLFLLEMSLKMYGMGPR----LYFHSSFNCFDFG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCWSCCSRSLP-WACE----- 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRAFMKLRRQQQ 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSKNRAYA-----IFFIVFTVIGSLFLMNLLTAIIYSQF------RGYLMKSLQTS 132
                                                                                                              2162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
   7.1%;
20.5%;
                                                                                                              244728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --HKWDPRSHLQPLAGTPEATYQMTVELLFRDILEEPGEDEL 471
   Score 186.5; DB 4; Pred. No. 5.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                              9D40173993B9E261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2162 AA.
                                    Length 2162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NFDTFPAA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341
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Search completed: October 8, 2002, 10:04:57 Job time: 72 secs